

FIGURE 1

ACTGCACCTCGGTCTATGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCCGGAGCAGCACGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCCGGCGCTGGGCTCCTGCCGTTCTGCTG
CTGCTGCCGCCGCCGGAGGCCAACAGAACGCCACCGCAAAGAACGAGCTGCCACCAGGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGACACCGCAAAGAACGAGCTTGGCGCGGGAAACA
CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATC
CTGGAGGGCTGTGCAGAGCAGCAGTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATCGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGAGATGGGAGCAGACA
GGCGACGGGTCCGCCGGTGCACATGGGTACCAGGGCCGCTGTGACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCAGTCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCCGGAGTGTGAAGTGGCTGGGTGCT
GGACGAGGGCGCCTGTGGATGTGGACAGTGTGCGGCCAGCCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGAAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGCCTCACTAGCAGAAAAACCTGTGTGAGGAAAAACG
AAAAGTGTACAATACTCCAGGGAGCTACGTCTGTGTGCTGACGGCTCGAAGAAACG
GAAGATGCCTGTGTGCCGCCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTACCCTTAAATTATTAGAAGGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCCGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCCTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATATTTGATACTAGTTCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAGGGCGCCGCGACTCTAGAGTCGACCTGCAGAACG
TTGCCGCCATGCCCAACTGTTATTGCAGCTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTCAAAATAAGCATTTCAGTCATTCTAGTTGTGGTTGTCAAAC
ATCAATGTATCTTATCATGTCGGATCGGGATTAAATTCCGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCGGAAGAACCGAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCAG
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAKKPTPCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHSICTACDESCKTCSGLTNRDCGECEVGWLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNKECISGYAREHGQCADVDEC SLAEKT
CVRKNENCYNTPGSYVCVPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAATGCACCTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACCGTCCGCCAGGCCGGAGGCACGCGCCAGCGTCAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGACTATCTGACGGGCCAGGTTGCGTAGGTGCG
GCACGGAGGAGTTTCCCGCAGCGAGGAGGTCCTGAGCACATGGCCCGGAGGAGCGCCTTC
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCTGTGCCTGCTGGCACTGCAGGCCGGAGGC
CGGGCCGCCGAGGAGGAGGCCTGTACCTATGGATCGATGCTCACCAGGAAAGAGTACTCA
TAGGATTGAAGAAGATATCCTGATTGTTCAGAGGGAAAATGGCACCTTTACACATGAT
TTCAGAAAAGCGAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTCTATGAATTCTGTCCCTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGAACAGTGCTCACAAGGCA
TCAGTTGTTCAAGTTGGTTCCATGTCTGGAAAACAGGATGGGGTGGCAGCATTGAAAGT
GGATGTGATTGTTATGAATTCTGAAGGAAACACCATTCTCAAACACCTCAAATGCTATCT
TCTTAAACATGTCAACAAAGCTGAGTCCCCAGGCCGGTGGCAAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCGAGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACCTGTGACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGACC
TGTTTCTACCCGGAAAATGTATTGCCCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCCAACCCGTGAAATGGAGGTAATGCATTGGAAAAGCAAATGTAAGTGT
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGGTGACAT
GGAACCTGCCATGAACCCAACAAATGCCATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGC
ACACGCCCTCACTTAAAAAGGCCAGGAGCGGCCGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTCATAGCCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATTATTAGCT
TCATTATAAAATCACTGAGCTGATATTACTCTTCTTTAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTCTTGTGCTTCAAGTGTGAGTTGGCAGATATTCTAAATTACAATGCATTG
TCAGGTTAAAATTTCAGTGTGAGTTGGCAGATATTCTAAATTACAATGCATTG
GTCTGGGGCAGGGAAACATCAGAAAGGTTAAATTGGCAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTCAGATTATTGTCAAGTATTAGAT
GTTTGTACATTAAAATTGCTTTAAACTCTCAATACAATATATTGACC
TTACCAATTCCAGAGATTCACTGAGTATTAAAAAAAAAAATTACACTGTGGTAGTGGCATT
AAACAATATAATATTCTAAACACAATGAAATAGGAATATAATGTATGAACTTTTGCAT
TGGCTTGAAGCAATATAATATTGTAACAAAACACAGCTTACCTAATAAACATT
ACTGTTGTATGTATAAAATAAAGGTGCTGCTTGTGTTGGAAAAA
AAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCAACTGTTATTGCAGCTTATAATG

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
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MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHCEKALCTPRCMNGLCVTPGFCICPPGFYGVNCDKANCST
TCFNNGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIKGSKCKCSKGYQGDLCSPVVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACCCGTGGCGTCCGGCGTCCGAGGCCAGGGAGGCCAGGGCGAGGCCAGGGCGCAGGCCAGCCTGGG
CCCCAGCCCACACCTCACCAAGGGCCAGGAGCCACC**AT**TGGCGATGTCCACTGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCACTTGGCTCTGGGTGCCAGCAGGGCTGTGGCGCCGG
GAGCTAGCACCGGTCTGCACCTGCGGGCATCCGGACGCCGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGCGTCCGACGACTGTGCCCTGCCCTACCTGGCGCCATCT
GTTACTGTGACCTCTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCCACCCCCCTTCCCCGATCCAAGGATGTATGCATGGAGGTGCTATCTA
TCCAGTCTGGAAACGTACTGGACAACGTAAACCGTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTCTGGGCATGACCTGGAT**GAGGGCATTGCTACCGCCTGGCACCA**
TCCGCCATCTCCTCGGTATGAAACATGCATGAAATTATACAGTGTGAACCCAGGGAG
GTGCTTCCCACAGCCTCGAGGCCCTGTGAGAAGTGGCCAACCTGATTGATGAGCCTTGA
CCAAGGCAACTGTGCAGGCTCTGGCCTCTCCACAGCAGCTGTGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCGTCTGCTCGCCAGAACCTGCTGTCTGTGAC
ACCCACCAGCAGCAGGGCTGCCCGGTCTCGATGGTGCCTGGTGGTCTCTGCGTCG
CCGAGGGGTGGTGTGACCACTGCTACCCCTCTCGGGCGGTGAACGAGACGGCTGGCC
CTGCGCCCTGTATGATGCACAGCGAGCCATGGGTGGGCAAGGCCAGGCCACTGCC
CACTGCCAACAGCTATGTTAAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGCCAACCTGGGCC
CAGCCTGGGGCGAGAGGGCCACTCCGCATCGCGCGCGTCAATGAGTGCAGACATCGAG
AGCTCGTGTGGCGTCTGGGCCCGTGGCATGGAGGACATGGGTCACTGAGGCTG
CGGGCACCACGCCGGCTGGGATCCAGGCTAAGGGCGGCCAGAGGCCCAATG
GGCGGTGACCCAGCCTCGCCGACAGAGCCGGCGCAGGCCAGGGCGCTAAT
CCCGCGCGGGTCCGCTGACGCAGGCCCGCTGGGAGCCCGGGCAGGCCAGACTGGCG
GAGCCCCAGACCTCCAGTGGGACGGGCGAGGCCCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCTCTGGGCCCAACTCAAGACTACAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCGTATTCTTTTTTTTTAGACAGGGTCTGCTCCG
TTGCCAGGTTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACCTCCACTCCTGGTTCA
AGTGCACCTCCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCACACCTGGC
TAATTGGTATTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCGAACT
CCTGGGCTCAAGCGGTCACCTGCCCTCCCAAAGTGTGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTCACTGTTAAAAA
TAAAACCAAAAGTATTGATAAAAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLLAGHLALGAQQGRGRRELAPGLHLRGIRDAAGGRYEQDLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTTNTGCNATCCGATTGTTGTCCTCAAATCCA
ATTCTCTTGGGACACATNACGCCGTCTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCTGCCTGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCATGGTCGGGCAAGGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCTATAAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTGGG
AGGCCAGAGAGATAACGCCGGCATGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACC CGCGCATCCCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAAC TCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGACCCGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCA GTGGGAGCCTGTCCTGGTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCCTGACCCCTCCCATGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCCTCCAACCCCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCACCCCTAACCCCTTAACCCCTGTGCTCAGGCACCTCTCCCCCAGGAAGCCTT
CCCTGCCAACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCCCTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTGTTGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCFHGPAGFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCGGAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGGCCAGCGGAAGAGCAAAGACTG
CGTGGTTACGGAGATCGTGCAGGAGAACAACTATACGGCCTTCCAGAACGCCGGCACGAGG
GCTGGTTACGGCCTTCACGCCAGGGCGGCCAGGCTTCCGCAGCCGCCAGAAC
CAGCGCGAGGCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAACGAGAACAGCAGTTCGAGTTGTGGCTCCGCCCCACCCGCCGGACCAAGCGCACAC
GGCGGCCAGGCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCTGGCCGCCTCCC
CACCCCTTCCCTTTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGAGCCAGATCCCC
GAGGGAGGACCCCTGAGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCTTCCGGACGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTCAACCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGGCCGGCTCCTGAAGCC
CGCTGAAAGGTCAAGCAGTGAAGGCCTGCAGACAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTGGATCTCCCTCAGTCTGCCCTCAGGAAAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTCAAGGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCAACTCCCAGCCC
CGGAATAAAACCATTTCCCTGC

FIGURE 11

MGAARLLPNLTLCQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRKGKLIGKPSGKS KDCVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTCATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTAC
CATACGCCCTCAGGACGTTCCCTAGCTGGAGTCTGGACTTCAACAGAACCCATCCAGT
CATTTGATTTGCTGTTATTTTTCTTTCCCACCATGTATTTAT
TTCCGTACTTCAGAAATGGGCTACAGACCACAAAGTGGCCAGCCATGGGCCTTTCC
GAAGTCTTGGCTTATCATTCCCTGGGCCTACTCACAGGTGCAAACACTCCTGGCCTGCC
CTAGTGTGTGCCGCTCGACAGGAACCTTGCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAAATGC
TGGATTCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCAAGAACATGTCAGAGTTCTCCATTGCAGGAAAAC
AAATATTCAAGACCATTACGGGCTGCTTGCCTCAGCTCTGAAGCTTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCCTCCGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAACATCCTGAGCAGTGTGCCTGTTGGCTTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAATCGAATTGCTGTCTATCCGACATGGCCTCCAGAA
TCTCACGAGCTTGGAGCGTCTATTGTGGACGGAACCTCTGACCAACAAGGGTATGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTAAGGAATTTCATTGTACGTAATTGCTGTCC
CACCCCTCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAGGACAACCAAGAT
AAACACATTCTTGACAGCCTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTCGGGATGCTGACTCAAGGGTTTGATAATCTCTCAACCTGAAGCAGCTC
ACTGCTCGGAATAACCCCTGGTTTGACTGAGTATTAAATGGGTACAGAACGGTCAA
ATATATCCCTCATCTCAACGTGCGGGTTCATGTGCCAAGGTCTGAACAAGTCCGGG
GGATGGCCGTAGGGATTAAATGAATCTTGTCCCTGCTCCACCGACCCCCGGCTG
CCTCTCTCACCCAGCCCCAAGTACAGCTCTCCGACCACCTCAGCCTCCCACCCCTCTAT
TCCAAACCCTAGCAGAACGCTACACGCCTCCAACCTTACACATCGAAACTCCCACGATT
CTGACTGGGATGGCAGAGAAAGAGTGAACCCACCTATTCTGAACGGATCCAGCTCTATC
CATTTGTGAATGATACTTCAAGTCAGCTGGCTCTCTCTTCAACCGTGTGGCATA
CAAACTCACATGGGTAAAATGGGCCACAGTTAGTAGGGGCATCGTTCAAGGAGCGCAG
TCAGCGGTGAGAACACACCTGAGCCTGGTTAACCTAGAGCCCCGATCCACCTATCGGATT
TGTTAGTGCCACTGGATGTTAACCTACCGCGCGGTAGAACAGACACCATTGTTCAAGGGC
CACCACCCATGCCTCTATCTGAACACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGCTTGTATGGGGCGCGGTGATATT
GTGCTGGTGGCTTGCTCAGCGTCTTGTGGCATATGCACAAAAGGGCGCTACACCTC
CCAGAAGTGGAAATACAACCGGGCGGGAAAGATGATTATTGCAGGCAGGCACCAAGA
AGGACAACCTCCATCTGGAGATGACAGAACCGAGTTTCAGATCGTCTCTTAAATAACGAT
CAACTCCTTAAAGGAGATTCAGACTGCAGCCCATTACACCCAAATGGGGCATTAAATT
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCAGACCTGGAGC
ACTGCCATACGTGAAGCCAGAGGCCAGCGTTATCAAGGCAGAACATTAGACTCTTGAGAA
CACACTCGTGTGTGCACATAAGACACGCAGATTACATTGATAATGTTACACAGATGCAT
TTGTGCATTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAGTG
CTATCTTCTATTCAAGTTAACAGTTAACAGTTGTAACCTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGAFFLKS~~WLI~~ISLGLYSQVS~~KLLACPSVCRCDRN~~FVYCNERSLTSVPLGIP
EGVT~~VLYLHN~~NQINNAGFPAELHNVQS~~VHTVYLYGNQLDEFPMNL~~PKNVRVLHLQENNIQT~~I~~
SRAALAQLLK~~EELH~~DDNS~~I~~STVGVEDGAFREAI~~SLKLLFLSKNH~~SSVPVGLPV~~DQELR~~
VDENRIAVISDMAFQNL~~TSLERL~~IVDGN~~LLTNKG~~IAEGTFS~~HLT~~K~~EF~~SIVRN~~SLSH~~PPPD
LPGTHLIRLYLQDNQINHI~~PLTAFSNRL~~K~~ERLD~~ISNNQ~~LRMLTQGVFDNL~~SNLK~~QLT~~TARNN
PWFCDCS~~IKWV~~TEWLKY~~I~~PSSLNVRGFM~~CQGPEQVRGM~~AVRELNM~~MLLSCPTTPGL~~PLFTP
APSTASPTTQP~~PTLSIPNPSRSY~~TPPT~~SKLPTIPDWDGR~~ERV~~T~~PP~~I~~SERIQLSIHFVND
TSIQVSWL~~SLFTV~~MA~~YKLTWVKM~~GHS~~LVGGIVQERIVSGE~~KQHLS~~LVNLE~~PR~~STYR~~ICLVPL
DAFNYRAVEDT~~ICSEAT~~THAS~~YLNNGSNT~~ASSHE~~QTTSHSMGSP~~FLLA~~GLIGGAVI~~FVLVVL
LSVFCWHMHKKGRY~~TSQWKYNR~~R~~RKDDYCEAGTKD~~N~~SILEM~~TETSFQIV~~VSLNND~~Q~~LLKG~~
DFRLQPIY~~TPNGGINYTDCHI~~P~~NNMRYCNS~~S~~VPD~~LEH~~CHT~~

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCTGCCCTCCCACGAGCG
ATCCCCGAGGAGAGCCGCGGGCCCTCGGCAGGGCGAAGAGGCCAGAGGAAGACCCGGTGGCTCGGCCCTGCC
TCGCTTCCCAGGCAGGGCTGCAGCCTTGCCCCCTTGTCTCGCCTGAAA**ATGGAAAAGATGCTCGCAGGCT**
GCTTTCTGCTGATCCTCGACAGATCGTCTCCTCCCTGCCAGGGCAGGGCAGGGCGGTACAGTGGGAGGTCCATCT
CTAGGGGCAGACAGCCTGGACACCACCCGAGACGGCCCTTCTGGAGAGTTCTGTGAGAACAAAGCAGGGCAGACC
TGGTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAGGGAGTTCATGTGGACA
TCTTGCAATTCTTGACATTGGTCTGTGATGTCACCCGAGTGGGGCTGCTCCAATATGGCAGCACTGTCAAGAAATG
AGTCTCCCTCAAGACCTCAAGAGGAAGTCGAGGGTGGAGCGTGTCAAGAGGATGCGGATCTGTCCACGG
GCACCATGACTGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTAGAACAGAGGGGGCCGGCCCTGA
GGGAGAATGTGCCACGGGTATAATGATCGTACAGATGGGAGACCTCAGGACTCCGTGGCCAGGTGGCTGCTA
AGGCACGGGACACGGGCATCCTAATCTTGCCATTGGTGTGGCCAGGTAGACTTCAACACCTGAAGTCCATTG
GGAGTGGCCCCATGAGGACCATGTCCTTGCCAAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTCC
AGAAGAAAGTTGTGCACGGCCACATGTGCAGCACCTGGAGCATAACTGTGCCACTCTGCATCAACATCCCTG
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGAGAATCCAGGATCTGT
GTGCCATGGAGGACCAACTGTGAGCAGCTCTGTGTGAATGTGCCGGCTCTCGTCTGCCAGTGTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGCTGTGACTACTGTGCCCTAGAAAACACGGATGTGAAC
ATGAGTGTGAAATGCTGATGGCTCCTACCTTGCCAGTGCATGAAGGATTGCTCTTAACCCAGATGAAAAAA
CGTGACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGTGTCACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCGAGGAGTGTGAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTGAACACGGAGATTCTCGTCTGCCAGTGTGTCAGAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGCTCCGGGGATTACTGCCCTGCTGAGTGACCATGGTGTGAATACTCCT
GTGTCACATGGACAGATCCTTGCCCTGCTGAGGGACACGTGCTCCGAGCGATGGGAAGACGTGTG
CAAAATTGGACTCTTGCTCTGGGGACACGGTTGTGAACATTGCTGTAAGCAGTGAAGGATTCTGTTGT
GCCAGTGCTTGAGGTTATAACTCCGTGAAGATGAGGAAAACCTGCGAGAAGGAAAGATGTCTGCCAAGCTATAG
ACCATGGCTGTGAACACATTGTCAGACTGACGACTCATACACGTGCGAGTGTGGAGGGATTCCGGCTCG
CTGAGGGATGGGAAACGGCTGGCAAGGAAGGATGTCAGTGCACATGGCTGCGAACACATTGGTGT
ATAATGGGAAATTCTACATCTGCAAATGCTCAGAGGGATTGTTCTAGTGAGGACGGAAGACGGTGCAGGAAAT
GCACTGAAGGCCAATTGACCTGGCTTGATGATGGATCCAAGAGTCTTGAGGAGAAGGAAATTGAGGTG
TGAAGCAGTTGCACTGGAATTATAGATTCTGACAATTCCCCAAAGCGCTCGAGTGGGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAACTCAGGCAAAGACATGAAAAAGCCGTGGCCC
ACATGAAATACATGGGAAAGGGCTTATGACTGGCTGGCCCTGAAACACATGTTGAGGAGAGTTTACCCAAAG
GAGAAGGGGCCAGGCCCTTCCACAAGGGTGCCAGAGCAGCCATTGTTCAACGAGGGCTCAGGATG
ACGTCTCCGAGTGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTTGAGTGTGGGGTAGGAAAGCCATTG
AGGAGGAACATACAAGAGATTGCTCTGAGCCCACAAACAAGCATCTCTTATGCGGAAGACTCAGCACAATGG
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCGGATGGAAGACAGGACTCTCCAG
CAGGGAACTGCCAAAACGGTCCAACAGCCAACAGAAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT
CCTGTTCTAATTTCAGTGCAACACAGATATCTGTTGAAGAAGACAATCTTACGGTCTACACAAAGCTTT
CCCATTCAACAAACCTTCAGGAAGCCCTTGAGGAAAGAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCAAACGAAGAAGTAAGAAAATTAAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGGCC
TGGAAAATGCCCTGAGATAACAGAT**TGAAGATTAGAAATCGCGACACATTGTTAGTCATTGTATCACGGATTACAAT**
GAACGCAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTG
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATAACACTAACTTGTATAAATTATCTAGGAAAAAAATCCT
TCAGAATTCTAAGATGAAATTACAGGTGAGAATGAATAAGCTATGCAAGGTATTGTAATATACTGTGGACAC
AACTTGCTTCTGCCCATCCTGCCATTGTGCAATCTCATTGACTATACGATAAAGTTGACAGTCTTACTT
CTGTAGAACACTGCCATAGGAAATGCTGTTTTGTACTGGACTTACCTTGATATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTACTTGGAACAAGTTGAGTTTTATACAATATTTACCACTTCAG

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRHARTHPOQTALLESCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIQVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNPVGSFVCQCYSGYA
LAEDGKRCVADYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKG
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGEQLCINTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSRGKTCAKLDSCALGDHGCE
HSCVSSEDSFVCQCFCFGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFR
LAEDGKRCRCKDVCKSTHGCEHICVNNNGNSYICKCSEGFLVLAEDGRRCKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDSILTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEEDNLLRSTQKLHSTKP
SGSPL EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCGCCACGCTCCGCCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCGCCGGCTGGGCCCTGACTCCGTCCGCCAGGGAGGGC
CATGATTCCCTCCCAGGGCCCTGGTACCAACTTGCTGCCGTTTGTCTGGCTGA
GTGCCCTCGGCCCTCGCGGGCCCAGCTGCAACTGCACCTGCCGCCAACGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTCTTCCAGCGTGGTACACCTGCACGGGAGGTGTCTC
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGTCACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCTCGGGCTGGAGGGTCTCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGCCACAGCATAAAACCT
TAGAACTCAATGTAATGGTTCTCCAGCTCCTCCATCCTGCCGTCTCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCATCCTCCAGACTTCTTGACCAGCATTAGATGTCACTCGTG
GGCTTTAACCTCACCAACCTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGCCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGTACCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCAACGCCGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGACCC
TTCCCTGTACCTCCGCACGAGCCCTGGCCACCCATGGCCCTCCAGGCCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT
GGGGCCCACCCCAACCAATATCCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAAGCTGGCTCTGGTAT**GATGAC**
CCCACCACTCATTGGCTAAAGGATTGGGCTCTCCTCTATAAGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC
TTTACTGTGGAAAACCACATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTCACTGGCTCCAGGC
CCCCTGATCTGACCCACCCATCTAACACCAACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTACGGCTGGCTGGTTAGGTTACTGGGCAGAGGATAGGAATCTC
TTATTAAAACATGAAATATGTGTTTTCTATTGCAAATTAAAGATAACATAA
TGTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPAPPSCRQLGVPHVGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAEDAIAPRTLPWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR
MGAVPVMPVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCGCTCCTAGGGTTTTCCACTTG
TTGAATTGTTCTATACTCAAATTGACCAAGACACCTGTCTCCAAATGCAAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGGAAATTTAACTCAGTCCTGTGGCGAAATGCTAATTGC
ACTAACACAGAAGGAAGTATTATTGTATGTGTACCTGGCTCAGATCCAGCAGTAACCA
AGACAGGTTACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGTGCCATT
TAGATAATGTCTGTATAGCTGAAATATTAAATAAAACTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATTAGCTGAATCATCTCATTACTAGGTACAAGAACAAACA
CTATCTCAGCCAAGGACACCCTTCTAACTCAACTCTTACTGAATTGTAAAACCCTGAAT
AATTGTCAAAGGGATACATTGAGTTGACAAAATTCAACGGATATAGCTCTCAAAGTTCTTTGAT
ACATCTACAAAAACTCATGCACACTGTTGAACAGCTACTTAAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTCTTTGAT
TCATATAACATGAAACATATTCATCCTCATATGAATATGGATGGAGACTACATAAATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTGCATT
AGAGTATTGGCCTTGCTTCATCTGACAACTTCTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCTAGTCATGAGCTCAAACCC
ACCCACATTATGAAACTTGAAAAATAACATTACATTAAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGCATTTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGAATCACCT
GACACATTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATT
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGCTTGCCATATGCATT
ACCTCTGGTTCTTCAGTGAAATTCAAAGCACCAGGACAACAATTCAAACAAATCTTGCTG
TAGCCTATTCTTGCTGAACTTGTTCTGTTGGGATCAATACAAACTAATAAGCTCT
TCTGTTCAATTCAATTGGCGGACTGCTACACTACTCTTTAGCTGCTTGCATGGATGTGC
ATTGAAGGCCATACATCTTATCTCATTGTTGTTGGCTATCTAACAAACAGGATTGGCA
CAAGAATTTTTATATCTTGGCTATCTAACAGCCAGCCGTGGTAGTTGGATTTCGGCAGCAC
TAGGATACAGATATTGGCACAACCAAAGTATGTTGGCTTAGCACCGAAAACAAC
TGGAGTTTATAGGACCAGCATGCCTAATCATTCTGTTAATCTCTGGCTTGGAGTCAT
CATATACAAAGTTTCGTCACACTGCAGGGTTGAAACCAGAAGTAGTTGCTTGAGAAC
TAAGGTCTTGCAAGAGGAGCCCTCGCTTTCTGTTCTCGGCACCACGGATCTT
GGGGTTCTCCATGTTGTCACGCATCAGGTTACAGCTACCTCTCACAGTCAGCAATGC
TTTCAGGGGATGTTATTCTGTGTTTATCTAGAAAGATTCAAGAAGAT
ATTACAGATTGTTCAAAATGTCCTGTTGGATGTTAAAGGTAACATAGAGAATG
GTGGATAATTACAACACTGCACAAAATAAAATTCCAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCCAATTATTAACACTAGACAAAAGTATTAAATCAGTTTCT
GTTTATGCTATAGGAACGTGAGATAATAAGGAAATTATGTATCATATAGATATACTATGT
TTTTCTATGUAAATAGTCTGTCAAAATAGTATTGAGATATTGGAAAGTAATTGGTT
CTCAGGAGTGATATCACTGCACCCAAGGAAAGATTCTCTAACACGAGAAGTATATGAA
TGTCCTGAAGGAAACCACTGGCTTGATATTCTGTGACTCGTGTGCTTGAAACTAGTCC
CCTACCACTCGGTAATGAGCTCATTACAGAAAGTGGAACATAAGAGAATGAAGGGCAGA
ATATCAAACAGTGAAAGGGAATGATAAGATGTATTGAAATGAACTGTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAACACATTACCACTTGTGAA
TTGTTCTGAACTAAATGTCCACTAAACAACTTAGACTCTGTTGCTAAATCTGTTCTT
TTTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVVFSTLLNCYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEYVYRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
SNTLTFVKTVNNFVQRDTFVWDKLSVNHRRTHTKLMHTVEQATLRISQSFQKTTEFDT
NSTDIALKVFFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSNGNVAVAFLYYSIGPLLS
SSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSRKVTDRYRSLCAF
WNYSPDTMNGWSSEGELTYSNETHTSCRNCNLTHFAILMSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCIIAGL
LHYFFLAFAFWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFYGLSPAVVVGFSAAALGYRYYGT
TKVCWLSTENNFIFSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVHLVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACCTGAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCCTCCCGCAGATCCGAACGGCCTGGCGGGGTCAACCCGGCTGGGA
CAAGAACGCCGCCCTGCCTGCCCGGGGCCGGGGCTGGGGCTGGGGCCGGAGGCAG
GGTGTGAGTGGGTGTGCGGGGGCGGAGGCTTGATGCAATCCGATAAGAAATGCTCGGG
TGTCTTGGCACCTACCGTGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCCGAG
CCGCCGCGCCGTCAGAGCAGGAGCGCTCGTCCAGGATCTAGGGCACGACCATCCAAACCC
GGCACTCACAGCCCCGAGCGCATCCGGTCGCCGCCAGCCTCCGCACCCCCATGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTTGTCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCGTGGCCGGCGCCCTCGCCTCTCGGACGCCGGGCC
CCACGTGCACTACGGCTGGGGGACCCCATCCGCTGCACCTGTACACCTCCGGCCCC
ACGGGCTCTCCAGCTGCTTCCTGCGCATCCGTGCCGACGGCGTCGTGGACTGCGCGGGGC
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
CGTGCACAGCGTGCCTGACCTCTGCATGGCGCCGACGGAAGATGCAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCGCCTCCGGTCTCCCTGAGCAGTCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTCTTCCACTCTCTCATTCTGCCTGGGAATCTGACATGTTCTCTCGCCCTGGAGACCGACAGCATG
AGGACCTCAGGGGCCACTTGGGAATCTGACATGTTCTCTCGCCCTGGAGACCGACAGCATG
GACCCATTGGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCCAGCTTGAGAAGTA
GAGACCATGCCGGGCTCTTCACTGCTGCCAGGGCTGGTACCTGCAGCGTGGGACG
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCAGTTCTAGCCAATAGACTTGCTGAT
CATAAACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGGCCCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGTTGAATACCTCCATCGATGGGAAC
TCACCTCCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTCTCATCACTTC
CCCAGGAGCAGCCAGAACAGGCAGTAGTTAATTCAAGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTCACTCAACCCATGTGGAATTGATCTATATCTACTTCCAGGG
ACCATTGCCCTCCCAAATCCCTCCAGGCCAGAACGACTGGAGCAGGCATGGCCACCAAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGGCCCTGGGACAACCTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTGAGAATAACTTGCTGTCCTGGTGTACCTGC
TTCCATCTCCAGGCCACCAGCCCTCTGCCACCTCACATGCCCTCCCATGGATTGGGGCCT
CCCAGGCCCCCACCCTATGTCAACCTGCACTTCTGTTCAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCAAGTCTTGTCAATAACTTGCTGTTGGAAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCAGCACTGGTTTCCAACATGATAATTATGAGTAATTATTTGATATGTACA
TCTCTTATTTCTTACATTATTATGCCCAAATTATATTATGTATGTAAGTGAGGTTG
TTTGTATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLES
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAACGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCGGAAAGATGGCAGGAGGAGCCGCCACCGCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCCAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGAAAACCCAA
AGAAGACTGTTCCCTCAGATTAGAGTGGAAAGAACTGGTCGGAGTGTCCCTTGCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAATGTGACAAGAAGTGTGATGCCGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG
AGCAAGGCCAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTTTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAAATCCAGCTCCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA
ATCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATACAAAAACTGGAAC
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCCGTGAAGCCCGCAATT
TGTTGGATATCGCAGGTGTCCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTAGTGATTCGTTGTGGCCTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTGAATGTGCAGTGGCTACGCCTGTAATCCAGCACTTGGAAAGG
CCGGCGGGCGGATACGAGGTAGGAGTTCTAGACCAGTCTGGCCAATATGGTAAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTAAAAAATAAAATAATA
AATAAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGI
LLENPRLGSQST
NSSYTMNTKTGTQFNTVSKLDTGEYSCEARN
SVGYRRCPGKRMQVDDLNISGIIAAVVVA
LVI
SVCGLGV
CYAQRKG
YFSKETSFQKS
NSSSKATTMSE
NVQWLTP
VIPALWKA
AAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGGCAACATTATTAACATGCTCCACAGCCGGACCCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGGATTAAATATTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTACATACATACTCCACCTCAAAAAGTACATCAATA
TTATATCATTAAGGAATAGTAACCTTCTCTCCAATATGCATGACATTGGACAATG
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGGTCTATGGCATTCA
TTTGACAAATGCAAGCATCTTCCTTATCAATCAGCTCTATTGAACTTACTGACTGACTG
TGGAATCCTTAAGGGCCCATTACATTCTGAAGAAGAAAGCTAAGTGAAGGACATGCCACT
CCGAATTCTATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCCAGCCAGATTGCC
AGCTAACACACAGATTCTCTCACAGACTAACAAATATTGCAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTATCTTCAGTCACCAAT
ATTAATGTAAGGAGATGCCTCAGCTCTTCTGTGTACCTAGAGGAAACAAACTTACTGA
ACTGCCCTGAAAATGTCTGTCCGAACTGAGCAACTACAAGAACTCTATATTAACTACA
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTCTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT
TCTGATGATTGGGAAAATCAAATTATCAGAACATCAAAGACATGAACCTTAAAGCCTTATCA
ATCTTCGCGAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACAGATAACGCCTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCATGT
TGCTCTCAAAGTGTAAATCTCAAATTGGATCTAAATAAAATCCTATTAAAGAA
TACGAAGGGGTGATTAGCAATATGCTACACTAAAAGAGTTGGGATAAAATAATGCT
GAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTAAAGAAAATAGAAC
TACTAACACCCCTAGATTGTCTACATTCAACCCATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATGGTACCATGAGTCT
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCATCAGGTGTGACTGTGTCATCCGTTG
GATGAACATGAACAAAACCAACATTGATTGAGCCAGATTCACTGTTTGCCTGGACC
CACCTGAATTCCAAGGTCAAATGTTGGCAAGTGCATTCAAGGACATGATGGAAATTGT
CTCCCTTCTTATAGCTCTGAGAGCTTCTTAATCTAAATGTAGAACAGCTGGAGCTATGT
TTCCTTCAGTGTAGAGCTACTGCGAGAACACAGCCTGAAATCTACTGGATAACACCTTCTG
GTCAAAACTCTGCCTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA
GATAAAATGGCGTAACTCCCAAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAAATG
GCTCTTGAATATTAAAATAAGAGATATTCAAGGCCAATTCAAGTTGGTGTCTGGAAAGCA
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTCGCAAAGTGCCTGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCACATCTACAGAAAAACAGAAAAAAA
TGTGTAAATGTCACCACCAAGGTTGACCCTGATCAAAAGAGTATGAAAAGAATAATAC
CACAAACACTTATGGCCTGTCTGGAGGCCCTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGATAAAATCTCTGGGAAGCAGGAAA
AGAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCT
AAAAACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRS IYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNAKIEYSTDFPVNLTGDLDSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELNSNLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRQMINSKWFDA
LPNLEFILMIGENPI IRIKDMNFKPLINLRSVIAGINLTEIPDNAVLGLENLESISFYDNRL
IKVPHVALQKVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNI RFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLGIIGVICLISCLSPEMCDGGHSYVRNYLQKPTFALGELYPP LIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGC**ATGAATCT**
GGTAGACCTGTGGTTAACCGTTCCCTCCATGTGTCCTCCTACAAAGTTTGTTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCTAAGGGCTGTCTTGTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTCAAAGGAGTAGCTGAAACCTTGAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAATGCCTTCATAACCTGAAGGCCAGGGCCAGAATTGCCAACAAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGAAAACGTCCGTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTGGCTGGTCACTATGGTATCTCATATGTGGTATATTGTGAGGCAAATCAGGAG
GATGCCGGAGACACCTCGAATACTTGAATCCCTGCCAAGCAGGAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGT**ATAGTGT**CCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTGCGATTGCACTAGAAATAAGTGGTTACTTCTCCATCATTGTAACACATTGAA
ACTTGTATTCAGTTTTTGAAATTATGCCACTGCTGAACTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTT
AATTAAAAGCAAATAAGCTTAACTTGAACCATTGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMC PKGCLSSSGGLNVTC SANLKEIPRDL
PPETVLLYLDNSNQITSIPNEIFKDLHQI RLVLNLSKNGIEFIDEHAFKGVAETLQTLDSL DNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASN HETAHN VICKTSVLDEHAGR PFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCAGGGCGCCCAGATGCAGGTGAGCAAGAGGAATGCTGGCGGG
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCCTGCTGGCAGCCCATCCTCTGCTGGTGC
GGGCTCAGTGTGTCAGGCTGGCCACGGCTGCCGCCGCTGCGAGTGCTCCGCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTGTGGCAGTCCCAGGGCATCCCCACCGAG
ACGCGCTGTGGACCTAGGCAAGAACCGCATCAAAACGCTAACACAGGACGAGTTGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTAACGAGAACATCGTGAGGCCGTGGAGGCCGG
CCTTCAACAACCTCTCAACCTCCGGACGCTGGCTCCGAGCAACGCCCTGAAGCTCATC
CCGCTAGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCGCGCCTCAGCGGCCTAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCGCTGTCCCACCTGCACGGCCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTCAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCCTACTTGGACACCATGACACCCAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCGTCCGCCACCTAGTCTATCTCGCTTCTCAACCTCTTACAACCCCCATCA
GCACCATTGAGGGCTCCATGTTGATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCAGCTGGCGTGGTGGAGCCCTATGCCTTCCGGCCTCAACTACCTGCGCGTGTCAA
TGTCTCTGGCAACCAGCTGACACACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCTGTGGTGTCCGG
CGCCGCTGGCGGCTCAACCTCAACCGGCAGCAGCCCACGTGCGCCACGCCAGTTGTCAA
GGGAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTTCACCTGCCCGCG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGGCACACGGTGCAGTT
GTGTGCCGGGCCATGGCGACCCGCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGGGCAACGCCGGCAACGAC
TCCATGCCGCCACCTGCATGTGCGCAGCTACTGCCACTGGCCCCATGCCAACAA
GACCTTCGCTTCATCTCAACCAGCGGGCGAGGGAGAGGCCAACAGCACCGGCCACTG
TGCCTTCCCTTCGACATCAAGACCCCATGCCACCCATGGCTCATCTCTTC
CTGGCGTGTCTCTGCTGGTGTGCTGTTCTGAGGCCGGCAAGGGCAACAC
AAAGCACACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
ACGCCGCCCCCAAGTCAACATGAAGATGATATGAGGCCGGCGGGGGCAGGGACCCCCG
GGCGGCCGGCAGGGGAAGGGCCTGGCGCCACCTGCTCACTCTCCAGTCTTCCACCTC
CTCCCTACCTTCTACACACGTTCTCTTCTCCCTCCGCCCTCGTCCCCCTGCTGCCCG
CCAGCCCTCACCACCTGCCCTCTTCTACCAAGGACCTCAGAACGCCAGACCTGGGACCCCA
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACAGCGGGCAGAGTCA
ATAATTCAATAAAAAGTTACGAACCTTCTGTAACTTGGTTCAATAATTATGGATT
TATGAAAATTGAAATAATAAAAAGAGAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL
GLRSNRKLIPLGVTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDLTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFNLNSYNPISTIEGSMILHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVNVSGNQLTTLEESVFHSVGNELETLILDSNPLA
CDCRLLWVFRRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLLEVRYAQVQDNGTYL
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCCACGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC
ATCGTAGTCCACCCCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTCGCCAGCGCCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGGCCCAAGCCGCTCGCTCCTGCTCCTGCTCCTGC
TGTCGCCTGCTGCTGGCGCCGGCGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGTCAAGTGCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCAAGCTGGTTACCTCTACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT
ATAAAATCTTCAATTACGGAAAAAGACACAGCCACCCCTAAACTGTCACTGTCTCTGGAGCAAG
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACCTCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAAACCTTCACTGTCAAGCTCGTCACTGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCCTGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAACGCTGTGCTACACTGTGAGGGTCGCCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCCAGCCACCA
CAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACCCAGTCCGGTGCCT
CCTCCTCCAGCACCTACCACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTTCCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACGTGACACA
TGAGGCAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGGC
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTCATAGAGGCGCCTGCCACTTCCTGC
GCCCCCCAGGGGCCCTGTGGGACTGCTGGGGCGTCACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCCCTCCCGCTTGCTCCAGCCCACCCACCCCGTACAGAATGTCTGC
TTGGGTGCGGTTTGACTCGGTTGGAATGGGGAGGGAGGGAGGGCGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGGCCCTGGGTGAGAAAAGCAAAAACA
AACAAAAAACAA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRQLVTSTPHELSIISNVALADEGEYTCSIFTMPVRTAKSLV
TVLGIIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTTCCTCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAATGCTGTTGGATTCTGTT
GCTGGAGACGTCTCTTGTGTTGCCGCTGGAACGTTACAGGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTTACCATTTATTCATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTTGCTAACCTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTTGATGAAATCGTCCGGGGCTTTCTGGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTCTGAAAGCAGACTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTAAATGACAATCTCATCAGCACCCACCTGCCAAC
GTGTTCCAGTATGTGCCCATACCCACCTCGACCTCCGGGTAAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCAGTGGTCTGCGAAGCCCCACCAAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCCTTGAAAAAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG
CCCAAGAAGAGACCTTGCTCTGGACCCCTGCCAACTCCTTCAAGACAAATGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCAGGCAACTGGCAGAT
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCAGGAACAAACCTTAGCTAAC
GTTTACCCCTGCCCTGGGGCTGCGACTCGACCATCCAGGGTGGTTAAAGATGAAC
TGCAACAAACAGGAACGTGAGCAGCTGGTGTGATTTGAAGCCAAGCTCTAACGTGCAGGA
GCTTTCTACGAGATAACAAGATCCACAGCATCCGAAATCGCACTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTTCAAG
AACCTTTGGACCTCAGGTGGTATACATGGATAGCAATTACCTGGACACGGCTGTCCGGGA
GAAATTGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAAACACCTG
CTGAGGTCCCTGCCGTGGACGTGTTCGCTGGGTCTCGCTCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGTGTGGACCAAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGAGTGCTCCTGCACAATTGTGCCCTTCAAGCAGTGGCA
GAACGCTTGGGTTCCAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTCT
TAGAAAGGATTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACCTGGCACAGTAAAACAGCACTGGGTGGCGAGACCCGGACGCCACTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTGGTGTGGCTGGACTGCTGCTGGT
GTTTGTACCTCCGCCTTCACCGTGGTGGCATGCTCGTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCTCCCGTCCGAGATTAAATTCCCTACAGACAGTCTGT
GACTCTTCTACTGGCACAATGGCCTTACAACGAGATGGGCCACAGAGTGTATGACTG
TGGCTCTACTCGCTCTCAGACTAAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAAGGCG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCGCG
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTGGCACAAACCGAAAGGGCCT
GACCCCTTAAGTAGCTCCCTCTGAAACAAAGAGCAGACTGTGAGAGCTGGAGAGCGCA
GCCAGCTCGCTCTTGCTGAGAGGCCCTTGTGACAGAAAGCCAGCACGACCCCTGCTGGAG
AACTGACAGTGCCTCGCCCTCGGCCCTGGCCCCGGGCCTGTGGGTTGGATGCCCGGTTCTATAC
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACCTTGACTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTCVCKEKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYHLFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPG AFLGLQLVKRLHINNNKIKSFRKQTFLGLDDLEYLQADFNLLRDIDPGAFQDLNKLEVILNDNLISTLPANVFQYVPITHDLRGNRLKTLPYEEVLEQIPGIAEILLEDPNWDCCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQGKDLNETTEQDLCPLKNRVDSSLPPAPAQEETFAPGPLPTPKTNGQEDHATPGSAPNGGKTI PGNWQIKIRPTAAIATGSSRNKPLANSLPCPGCSDHIPGSGLKMNCNNRNVSSLADLKPKLSNVQELFLRDNIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNYLDTLSREKFAGLQNLEYLNVEYNALIQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSLSKLSHNMYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKCETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHNSYLDTSRVSISVLPVGLLVFVTSAFTVVGMLVFILRNRKRSKRRDANSSASEINSLQTVCDSSYWHNGPYNADGAHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577, 608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349, 354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTCGTCCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCTGTGCGGCCCTAAGGGAAACTGTTGGC
CGCTGGGCCCGGGGGATTCTGGCAGTTGGGGTCCGTCGGGAGCGAGGGCGGAGGG
AAGGGAGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTGTGGAGCAGCTGCGTGCGGGCCTCAG
AGAATGAGGCCGGCGTTCGCCCTGTGCCCTCTGGCAGGCCTCTGGCCCGGCCGGCG
CGCGAACACCCCCACTGCCGACCGTGCTGGCTGCTCGGCCCTCGGGGCTGCTACAGCCTGC
ACCAAGCTACCATGAAGCGGCAGCGGGCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCGGGCGCCAGCTGCGCCTGTGCTCGCGCTCTGCGGGCAGGCCAGG
GCCCGAGGGGCTCAAAGACCTGCTGTTCTGGGTGCACTGGAGCGCAGGCCTTCCACT
GCACCCCTGGAGAACGAGCCTTGCAGGGTTTCTCCTGGCTGTCCTCCGACCCCGCGGTCTC
GAAAGCGACACGCTGCAGTGGTGGAGGAGCCCCAACGCTCCTGCACCGCGGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGTGAGGCCGAGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTGTGTCCTGCGCCGCCCCGG
GCCGCCTCTAACCTGAGCTATCGCGCCCTTCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTGCGCTCGCCGGGACAGCTCCCGATCTCAGTTACTGCA
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTGTCCTGCCCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACAGCCTAGACGACTGGGAGG
CTTGCCTGCGAATGTGCTACGGGCTCGAGCTGGGAAGGACGGCCGCTTGTGACCA
GTGGGGAAAGGACAGCCGACCCCTGGGGGACCGGGGTGCCACCAGCGCCGGCCACT
GCAACCAGCCCCGTGCCGAGAGAACATGGCAATCAGGGTCGACGAGAACGACTGGGAGAGAC
ACCACTGTCCTGAACAAGACAATTCAAGTAACATCTATTCTGAGATTCTCGATGGGAT
CACAGAGCACGATGTCTACCCCTCAAATGTCCTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTCCAAGTTAAATTCTACGACTCCTCTGCCACTCCTCAGGCTT
CGACTCCTCTCTGCCGTGGCTTCATATTGTGAGCACAGCAGTAGTAGTGTGTTGGTGTCT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCAGAAAGCCCTCTTCCAGCCA
AGGAAGGAGTCTATGGGCCGCCGGCTGGAGAGTGTGATCTGAGCCGCTGCTTGGGCTC
CAGTTCTGCACATTGCACAAACAATGGGTGAAAGTCGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCTTGTGGCGAGTCCCTCTGGCTCTAGTGATGCATAGGAAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGGAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGTGAACTGGGGACCGGGTAGTGCTGGGAGAGATATTTCTATGTTATTGGAGAA
TTGGAGAAGTGATTGAACCTTCAAGACATTGAAACAAATAGAACACAAATATAATTACA
TTAAAAAATAATTCTACCAAAATGGAAAGGAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTGAAATCCCAGGGAAAAAATAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPAGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGL
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCYQFEVLCPAPRPG
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGFFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR
KESMGPPGLES DPEPAALGSSSAHCTNNGVKVGCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGATTAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGAAACTAAG
CGTCGAGTCAGACGGACCATAATCGCCTTAAAAGTGCCTCCGCCCTGCCGGCGTATC
CCCCGGCTACCTGGGCCGCCCGCGCGGTGCGCGTGTGAGAGGGAGCGCGCGGGCAGCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCCGTGTGAGCGCGTGGGTGCGGA
GGGGCGTGTGTGCCGGCGCGCGCGTGGGTGCAAACCCGAGCGTCTACGCTGCCATGA
GGGGCGCGAACGCCCTGGCGCCACTCTGCCTGCTGGCTGCCGCCACCCAGCTCTCGCG
CAGCAGTCCCCAGAGAGACCTGTTCACATGTGGTGGCATTCTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCCTGGAGTGTACCCCTCCAAATAGCAAATGTACTTGGAAAATCA
CAGTTCCCAGGGAAAAGTAGTCGTTCTCAATTCCGATTCACTAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGCCAGCGCATTGGCG
CTTCTGTGGCACTTCCGGCTGGAGGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGTGCCAACACAGCTGGCAATGGCTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC
CCCCAACTGGCCAGACCGGGATTACCCCTGCAGGAGTCACTTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCACAGATGCTAGAAGAATTGGAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTTATTCACT
TTTATCAGACTTAAGTTAAC TGCAAGATGGGTTATTGGTCACTACATATTCAAGGCCAAA
AAACTGCCTACAACATACAGAACAGCCTGTCAACCACCATCCCTGTAACCACGGGTTAAA
ACCCACCGTGGCCTGTGTCAACAAAAGTGTAGACGGAGGGACTCTGGAGGGCAATTATT
GTTCAAGTGAATTGTGTTAAC TGCAAGATGGGTTATTGGTCACTACATATTCAAGGCCAAA
CACGCCACAGTCTCGATCATCACACATCACAAAGAGGGAAATTGGCGATTCAAGCAGGCC
CAAGAACATGAGTGCAGGCTGACTGTCGTCTGCAAGCAGTGCCTCTCCTCAGAACAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGCGAGGAAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAACATCAGAACGCTCTGGATGCCCTAAAAAATAAGCAATG
TTAACAGTGAACGTGTCATTAAAGCTGTATTCTGCCATTGCCCTTGAAAGATCTATGTT
TCTCAGTAGAAAAAAATCTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTCACATGATGGAGGTATGAGGCCCTCGAGATAGCTGAGGGAAAGTTCTT
TGCCTGCTGTCAGAGGAGCAGCTATGATTGGAAACCTGCCGACTTAGTGCCTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTGGAAAGCTTATTACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAAGATTTAGAAGTGCACATTATAGT
GTTATTGTTCACCTCAAGCCTTGCCCTGAGGTGTTACAATCTGTCTGCCTTCTA
AATCAATGCTTAATAAAATTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNDLCRYDFDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLDRPSGSFKTPNWPDYDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGEVNDARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTIIRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMQVGVEDGRGKIMPNSFIMMFKT KNQKL DALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACCGCGTGGCGGACCGCGTGGCGGCCACGGCGCCCGGGCTGGGCCTCGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTCAACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGACAACATTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGAACAGAGAGAGGCCCTGCCGTGGCTACGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGTACGGGGTGAGGCCTGTGGCC
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGGCATCTGGTATGTTGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGGTCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAAC
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA
ACAAGCAGTGTAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTCTTCAGAGATGAC
AGAAGACGAGTTGGTGGTGCAGCGCAGTGACCGTGTGGCTGGAGGGCTTCATCAAGGGCAGA
TACCGGGCCACCACTGTAGGACCTCCCACCCACGCTGCCCGAGAGCTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTGGTTATTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTTCCACCTGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCCAGTTCTGT
TCTGTGTTACCCACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQQSSPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPAGTERPCGGYGCCEGTRGGSGHCDCQAG
YGGEACGQCGLGYFEAERNASHLVC SACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVMTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAKGDLVFTAIFIGAVAAMTGYWL SERSDRVLEGF IKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCCTTGCTCCCTCCAGGGCA
GCACCATGCAGCCCCTGGCTCTGCTGGCACTCTGGGTGTTGCCCTGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTCAGCTCAAAGAGGT
GCCCACCCCTGGACAGGGCGACATGGAGGAGCTGGTATCCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCTGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCCCTTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGCGGCTGTCCCCCGCAGCGCCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCCGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCGCTGGCGTCCGGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGCCGAGAACTGGGTGCTGGAGGCCCGGGCTT
CCTGGCTTATGAGTGTGGCACCTGCCGGAGCCCCGGAGGCCCTGGCCTTAAGTGGC
CGTTCTGGGCCTCGACAGTCATGCCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCTGCCAGGGCTCCAGCCATGGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTGCAGGGTACCAAGGAGAGCTG
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTGGCTCTCAGGAATGAGAAATCTTGGCCACTGGA
GAGCCCTGCTCAGTTCTTCTATTCTTACTGCACTATATTCTAAGCACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTACTTGTCCGTAC
TGGATCTGGCTAAAGTCCTCCACCACACTCTGGACCTAACGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTTGAAAACATGAATAAACACATTTTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQVSQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGCGGCTGTTGTCAGTGGCCTGATCGCGATGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTCCTCTCATATTGGCGATCCTGTTGCTCCCTGG
CATTGGGCAGTGTTACAGTCACCTCTGAACCTGAAGTCAGAATTCCCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAAAGTTGACCA
AGGAGACACCACCAGACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG
TGACCTTCTTGCCAACGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCCTCCATCCAAGCCTACAGTTAACATCCCTCCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTTCTGAATAACACACTGGTTCAAAGAT
GGGATAGTGTGCTACGAATCCAAAAGCACCCGTGCCCTCAGCAACTCTCCTATGTCCT
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCTGTCAGCCTCTGATAACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGCATGGAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTTGTAAACCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCTTACT
CAGGTGCTACCGACTCTGGCCCTGATGTCAGTTCACAGGATGCCCTATTGTCCTTC
TACACCCACAGGCCCTACTTCTCGGATGTTAAATAATGTCAGCTATGTGCC
ATCCTCCTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACTTGTAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTCTGGCTCTTCTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGATTAGAGGCTAGAGCGGCTGAAATGGTTGG
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGCTTCCATGGGAAGTG
CCACTGGGATCCCTGCCCCTGCTCTGAATACAAGCTGACTGACATTGACTGTGCTGT
GGAAAATGGAGCTCTGTTGAGAGAGCATAGTAAATTTCAGAGAACTTGAAGC
GATTAAAACCGCTGCTAAAGAAAAGAAAATGGAGGCTGGCGCAGTGGCTCACGCC
TAATCCCAGAGGCTGAGGCAGGCCATCACCTGAGGTCGGAGTTGGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPEYTWFKDGI VMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGGCCCCAGCTCAG
GCTCGTGCACCCCACCAAGTCCAGTGCCGACCAGTGGCTTATGCGTGCCCCTCACCTGG
CGCTCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCACCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCCTGTGGAAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAACTGCCATGGGTTATTGCAGCTGCTGCCGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCTTGTCCCTGGCTCCGAGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC
CTCGCTGCCTGAGGACAAGCACTGCCACCCGTCACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGACACCCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAAACCTGCCACAGCCAGAACAGAC
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDCSDGSDEEECRIEPCQKGQCPPPGLPCPCTGVSDCSGGTDKKL
RNCSRLLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELCGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPSVGNATSSAGDQSGSPTAYGVIAAAAVLSASLVATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACCGCGTCCGGTCTCGCTCGCGCAGCGGCCAGCAGAGGTGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTGCAAGCTGGATGCCCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCACCTCAGTCCCCCAGAGACTCTG
GCCGTGATCCTGTGGTTTCAGCTGGCGTGTGCTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTTCAAGTGTGCTGACCCGGCATTCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAAGGCTCTGTAGCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAAGCTAACATCACTTGTATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCAATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTAATGGCTATGTAACATCTCTGAGC
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGTCTCGTATCTTGAGTGCTTACAAAACCTTATCTGGCGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCCAATGGTAGTCACGGAGATTCGTCT
GCCACCCGCGCCTTGTGAGCGTACAACCACGGAACGTGGTAGTTACTGCGATCCT
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGGTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCCGGAG
TTCCAGCAGTGAACCTGACTTTGTGGTAGACGGCGTCCGTATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGCTTGAGTGCTTAGGCCCGGTACATGGCTCTGTGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTGAGCTGCTCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCTGCTGGACAAACCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAAAAATTCCAAAGTGTCTGAAGTGTCTCTCAA
ATACATGTTGATCTGTGGAGTTGATTCCCTTCTCTTGTTAGACAAATGTAAACAA
AGCTCTGATCCTAAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTTGTCAAGTC
CTGTTCTTCTTGACACAGACTGATTAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPIQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAEEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCACCGCGTCCGCTCCCGCCCTCCCCCGCCTCCCGTGCAGTCGGTCCGTGGCTAGAGA
TGCTGCTGCCCGGGTTGCAGTTGTCGCACGCCCTGCCGCCAGCCGCTCCACCGCCGT
AGCAGCCGAGTGTCGGGGGGCGCACCCGAGTCGGGCCATGAGGCGGGAACCGCGTACAGG
CCGTGCTGCTGGCGTGCCTGGTGGGCTGCCGCCGACGGGCTGCTGAGTGCC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA
TAAAGTCATTACTTCCATGATACTTCTGAAGACTGAACCTTGAGGAAGCAAAGAACCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTCATTGAAAACCTTCCATCTGATGGTACCTCTGGATTGGCTCAGGAGGCGTGA
GGAGAAAACAAGCAATAGCACAGCCTGCCAGGACCTTATGCTTGGACTGATGGCAGCATAT
CACAATTAGGAACTGGTATGGATGCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACATTTCATTGCAAATATTCTGATGAGAACACCAGCAGTCCT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTCCAGAAGAACACAG
GAAGAACATGCCAAAAAAACATTAAAGAAAGTAGAGAACAGCTGCCTGAATCTGGCCTACAT
CCTAATCCCCAGCATTCCCCTCTCCTCCTGTGGTACCCAGTGTACTGTTGGTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCATC
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAACATTTCATTCCAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAATGGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAATC
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGAACAAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTGGCTGTATCCTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAACGGTACCTTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCACTGGTTGGTTGTATCTAACTTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGCTGTGGAGCTGGAAAACCACCTCTGTTTGCTCTATACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAGA
GCAGGAAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDDLRLGGQPVCRGQTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIKEFIENLLPSDGDFWIGLRRREEQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAALNAYILIPSIPLLLL
VTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSEGFTLVSVESGFVTNDIYEFSQDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGCCGGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTTGCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTGCGTTGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAACTC
AGTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTTGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAAAGTCTTGTATCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGTGATAAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCGGGATTTTGACCACAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCAGAGGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAEQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIHTDEADSEVLYPNYQSCWSLRQRTRGRRTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLPSMPLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLIES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELEYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCP LDMLNAMS VYTLSPEKYHALCSQTQVM EVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTGGGGACCTCCTCTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTGGTC**ATGG**CTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGGCGCTGGTGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGACCGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCCA
GTCCCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGAA
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGATGTGGAGGGCTGTACTGACTAAAAACGCTGCAACAAGCATGCC
TATGCCGAAAACCCATCTGGCTGAGCCAGATGTCACTGCTCAGGACGAGAAGCAACCCTCA
GGATTGCCCTCTGGCCTGGGGAAAGAACACCTGCAACCAGATGAAGACACGTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG
GAGGTGCTGACAAGGGCGTATGGGCTCTGTGTGATGACAACCTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGCTGGGAAGTCCCTCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGCCGCATCTGGCTGGATAATGTTGTTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTGGGTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGT**TAGGT**GGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTATACTTGTTGCCCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACATACATCA
CCACCTTCCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTAT
CAACTACTTAAATAACATTCTCACACACACACACACACACACACACACACACACACATA
CACCAATTGTCCTGTTCTGAAAGAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTATTTACAATAATAAGATAGCAC
TATGTGTTCAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQGTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVHLKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGCGTCCGGACCGTGGCGGACCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGGG
CGTCTCGGCCTCTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCAAGTGG
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCCAGTTGCTTAACGAAAGCACTCC
TGCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGTCGCGGCCAGATGAAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCAGGATGGATCTAGGTATGGAGTTATGGAC
ACCACACAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGTGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTCCTGGCTGTTATCTCGAA
CTCTGGCTCTGGCTCTTCTTCAGCCTCATGCCCTCCAGGGCCAGAAAGAGCGGAAATCC
AAGAACTCCT**AGT**ACTCTGACCAGCCAGGGCAGGGCAGAGAACGAGCACTCTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGCTCACAAGTGG
AAAGACTGAAGAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAGGGCGGCCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCAATTGTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLGCLGVFGLFRLLQWVRGKAYLRNAVVTGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI
VAAAAEILQCFGYVDIL
VNNAGISYRGTIMDTTVVDKRMETNYFGPVALTKALLPSMIKRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKS KNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCCACCGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTCTTCTGGACATCCTC
CTGCTTCTCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA
GAGGAGAAAATCAGTCACCGGCAGAACATCGTGTGATTACAGGAGCTGGCATGGAATTGG
GACTGACTGCCTATGAATTGCTAAACTTAAAGCAAGCTGGTCTCTGGGATATAAAATAG
CATGGACTGGAGGAAACAGCTGCCAATGCAAGGGACTGGGTGCCAAGGTCATACCTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTAATTGCACATTCTGGACTACAAA
GGCATTCTCCTGCAATGACGAAGAATAACCATGCCATTGTCACTGTGGCTCGCAG
CTGGACATGTCTCGTCCCCTCTTACTGGCTTACTGTTCAAGCAAGTTGCTGCTGTTGGA
TTTCATAAAACTTGACAGATGAAGTGGCTGCCTACAAATACTGGAGTCAAAACAATG
TCTGTGTCCTAATTGTAACACTGGCTTACTGTTCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTCTATAGCTTTTAACAACATTGAAAGGATCCTCCTGAGCGTT
CCTGGCAGTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAAAGCACCTAGTTCTGAAAACGATTTACCAAGGTTAGGTTAGTCATCTA
ATAGGCCAGAATTAAATGTTGAACCTCTGTTCTAATTATCCCCATTCTCAATA
TCATTGGAGGCTTGGCAGTCTCATTACTACCACTTGTCTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGCTTGCAA
AATTGTACCATACCGTTATTAAACATATATTATTATTGATTGACTAAATTGTTG
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTCAAGCTCTAAATAAAA
TGAAGGACTATATCTAGGGTATTCAACATGAATATCATGAACCTCAATGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTCTGAGAGATAACCTCACATTCAAGGCAAACATTCT
GCACAGGGAAGCTAGAGGTGGATACAGTGTGCAAGTATAAAAGCATCACTGGGATTAAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAA
AAAAAA
AAAAAA

FIGURE 58

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKGLGAKVHTFVVDCSNREDIYSSAKKVAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCACCGCGTCCGGACGCGTGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGGCTC
AGGGAGGAGCACCGACTCGCGCCACCCCTGAGAGA**GATGGTTGGTGCCATGTGGAAGGTGATTG**
TTTCGCTGGTCTGTTGATGCCTGGCCCTGTGATGGGCTGTTGCTCCCTACAGAAGT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTCTCACCCCTAACATTGAAGC
TGGGAAGATCAAAAAGGAAGAGAATTGAGTTGGTCGGCCCTTCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCTCACCGTAATAAGACTTACAACAGCAACCTCTCTGGTTC
TTCCCAGCTCAGATACAGCCAGAAGATGCCAGTAGTTCTCTGGCTACAGGGTGGCCGG
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGGCTTATGTTGTCACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTACTGATGATAACCACGGATATGCACTGAATGAGGAGATGT
AGCACGGGATTATACAGTCATAATTCAAGTTCCAGATATTCTGAATATAAAAATA
ATGACTTTATGTCAGTGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCGACTTAAC
AAAGTGATCCTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTGCCTG
GCACCGAACCTGAGGATCAGCTTACTATGTGAAATTGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGAACTATAGTTGAAAAGTACTTGCAGA
AGATACAGTACAGTCAGTTAACCATGGTTAAGGAACTGAAATCATGAATAATTAAAGGTTCTGA
TCTACAATGGCCAATGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTACCTTACCATGACCAGCCTCTGAGAGCTTTGACATGATTAATCGA
TTCATTATGAAAAGGATGGATGGATCCTTATGTTGAA**AAACTACCTTCCC**AAAAGAGAACAT
CAGAGGTTTATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTCATCAATAAAATTATCCTTGAAACAAGTGAGC
TTTTGTTTGGGGGAGATGTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTAGGGCTTGAATAGGAAGTTTAATTCTCTAACAGAGTAAGTGAAGAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT
GTTGGAAATTATTGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAACATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGREL
SVPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFEILDKLLGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTCCGGCTCCGGAATGGCACATGTGGAATCCCAGTCTTGGCTACAACAT
TTTCCCTTCCTAACAGTTAACAGCTGTTAACAGCTAGTGATCAGGGGTTCTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTACCGAGCTCCTT
CCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCTGCCAACAGCTTCAAAAAACAGGAGCGACTTCACTGGCTGGGAT
AAGACGTGCCGGTAGGATAGGAAGACTGGGTTAGTCCTAACATTGACTGGCTGGG
TGAACCTAACAGCCTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGCCAGAAA
TAGAGATGCTTGTAAAATAAAATTAAAAAGCAAGTATTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGAGGAGAAAGTATGTTAAAATA
GAAAAACCAAAATGCGAGAAGGAGGAGACTCACAGAGCTAACACCAGGATGGGACCTGGTC
AGGCCAGCCTTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCTGTGTTT
GCAGAACATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCTGGAGGTGG
ACAGCCGCTGTGGCTCTCAGTGGCTGGGTGCTGCTGGCCCCCCCAGCAGCCGGC
ATGCCTCAGTCAGCACCTCACTCTGAGAACATCGTACTGGACCTCAACCACCTGACCGT
CCACCAAGGGACGGGGCGTCTATGTGGGGCCATCAACCGGGCTATAAGCTGACAGGCA
ACCTGACCATCCAGTGGCTATAAGACAGGGCAGAACAGGACAACAAGTCTCGTTACCCG
CCCCCATCGTGAGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGCTTGCA
AGCTGCTGCGCTGGATGACCTCTCATCCTGGAGCCATCCCACAAGAACAGGAGCACTAC
CTGTCCAGTGTCAACAAGACAGGGCACCAGTACGGGGTGAATTGTGCGCTCTGAGGGTGGAGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCTGTCCA
GCCGGAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGCTCTCCACTTGACAT
CTTCTACATCTACGGTTGCTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA
CCCCGTAGGGTGTGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATCGTGC
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGTCCCTGCCCTCGGCTGCACCCGGC
CGGGGTGGAATACCGCCTCTGCAGGCTGCTACCTGGCCAAGCCTGGGACTCACTGGCC
AGGCCTCAATATCACCAGCCAGGACGATGTACTCTTGCCTCTCCATCTCCAAAGGGCAGAAG
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGTGCCTCCATCCGGGCCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCTGCTACCAAGGGCAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCTGTCCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCTGACCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGGACTAAGAGTGGCAAGTGAAGAAAGGTAAAGAGTCTATGAGTTAGCTAGATGCTCCAATGCC
ATTCACCTCCTCAGCAAAGAGTCCCTTGGAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTATTTCTGGGAACAAAGGTGAATGGGGAGGTAAGAACGGGTTAATTGAG
ACTTAGCTTCTAGCTACTTCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCCAAACCTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVVLLAPPAAGMPQFSTFHSENRDWTFNHLTQHQGTGAVYVGAINRV
YKL TGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLIACGSL
YQGVCKLLRLDDLFLVEPHKKEHYLSSVNKTGTMYGVIVRSEGEGDKLFIGTAVDGKQDY
FPTLSSRKLP RDPESSAMLDYELHSDFVSSLIKI PSDLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSL A QAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEQN
LELNWLLGKD VQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEG SYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGC GGACTGGAGTGGAAACCCGGGTCCCCCGCGTTAGAGAACACGCG**A**TGACCA
CGTGGAGCCTCCGGCGGAGGCCGGCCCGCACGCTGGACTCCTGCTGGTCGTTGGGCTTCTGGTGCCTCC
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGCGGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTCTGGATCTTGGGGCTCCATCCACTATTTCCGTGTGCCAGGGAGTACT
GGAGGGACCGCCTGCTGAAGATGAAGGCCTGTTGAACACCCCTACCCACCTATGTTCCGTGGAACCTGCATG
AGCCAGAAAGAGGCAAATTGACTTCTGGAACTCTGGACCTGGAGGCCCTCGTCCCTGATGGCCGAGAGATCG
GGCTGTGGGTGATTCTCGCTCCAGGCCCTACATCTGCAGTGAGATGGACCTCGGGGCTTGCCCAGCTGGCTAC
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTAACAGGGCTTCACCGAAGCAGTGGACCTTATTGACCACC
TGATGTCAGGGTGGTGCCTACCCAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAAGGTGAGAAATGAATATG
GTTCCATAATAAGACCCCGCATACATGCCCTACGTCAAGAAGGGACTGGAGGACCGTGGCATTGTGGAACCTGC
TCCTGACTTCAGACAACAGGATGGCTGAGCAAGGGATTGTCCAGGGAGTCTTGGGACCATCAACTTGCAGT
CAACACACGAGCTGCAGCTACTGACCAACCTTCTCTTCAACGTCCAGGGAGCTCAGCCCAAGATGGTGTGGAGT
ACTGGACGGGGTGGTTGACTCGTGGGAGGCCCTACAATATCTTGGATTCTCTGAGGTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGGCTCTCCATCAACCTCTACATGTTCCACGGAGGACCAACTTGGCTTCATGAATG
GAGCCATGCACTCCATGACTACAAGTCAGATGTCAACAGCTATGACTATGATGCTGTGCTGACAGAACCGGGCG
ATTACACGGCCAAGTACATGAAGCTCGAGACTTCTGGCTCCATCTCAGGCATCCCTCTCCTCCCCACCTG
ACCTTCTTCCAAGATGCCGTATGAGCCCTAACGCCAGTCTGTACCTGTCCTGTGGGACGCCCTCAAGTACC
TGGGGGAGCCAATCAAGCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCCT
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATGGGGCAGG
TGTGGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATTGCTGTGCTCCCTGATCCAGGGTT
ACACCGTGTGAGGATCTGGTGGAGAATCGTGGCGAGTCAACTATGGGGAGAAATTGATGACCAGCGCAAAG
GCTTAATTGGAAATCTCTATGAAATGATTCAACCTGAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTCAGAGGTTGGCTGGACAAATGGNTTCCCTCCAGAAACACCCACATTACCTGCTTCTTGG
TAGCTTGTCCATCAGCTCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGAGAAGGGGTTGATTCA
TCAATGCCAGAACCTGGACGTTACTGGAACATTGGACCCAGAACAGCCTTACCTCCAGGTCCCTGGTTGA
GCAGCGGAATCAACCAGGTACGTTTGAGGAGACGATGGGGCCCTGCATTACAGTTACGGAAACCCCCC
ACCTGGCAGGAACCAAGTACATT**G**AGCGGTGGCACCCCTCTGCTGGTGCAGTGGGAGACTGCCGCCTC
CTCTTGACCTGAAGCCTGGCTGCTGCCCAACCCCTCACTGAAAAGCATCTCTTAAGTAGCAACCTCAGGG
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTCAAAACCTAAGCCTGCCAGGGAAAGGTGGATGGCTTGGGCC
TGGCTTGTGATGATGGCTTCTCACGCCCTGCTCTGTGCCAGGGCTGTGGCTCTGACAGCTCACAGCCC
AGCTAATCAGATGCCCTGGACTCAGGGCTGCTCTTGCTGGTCTGGGAGGCTTGGCCACATCCCTCATGGCCCC
TGCGAGCATCTGCTGGACTCAGGGCTGCTCTTGCTGGTCTGGGAGGCTTGGCCACATCCCTCATGGCCCC
TTTATCCCCGAATCCTGGGTGTGTCACAGCTGAGGGTGGGGAAAGGGGTGTCACCTGAGCTGACTTGGTT
CTTCCTTACAACCTCTGAGCTTCTTGGGATTCTGGAGGAACCTGGCGTGAAGAACATGTGACTTCCCC
TCCCTCCACTCGCTGCTTCCCACAGGGTACAGGGCTGGAGAAACAGAACATCCCTACCCCTGCCTTCC
CAAGTTAGCAGGTGTCTGGTGTGTCAGTGAGGAGGACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGCA
CATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGACATCC
AGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGACATCCAGGG
GGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGACATCCAGGGAGGAGG
ACAGAACGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCACGCCGAACAGCAGGGCAGAGCAGGCCCTCCTTC
GAAGTGTGTCAGTCCGCAATTGAGCCTGTTCTGGGCCCCAGCCAAACACCTGGCTTGGCTCACTGCTGA
GTTGCAAGTAAAGCTATAACCTTGAATACAA

FIGURE 64

MTTWSLRRR PART LGLLL VV LGFL VL RRL DWST LVPL RL RHRQL GLQAK GWN F MLED ST FW
I FGGSI HYFR VP REYWR DR LLK MKAC GLNT LTT YVP WNLHE PERG KFDFSGN LDLE A FVL MA
AEIGLW VILR PG PYIC SEMD LGG LPSW LLQD PGM RLRT TYKG FTEA VDLYFDH LMSRV VPL Q
YKRGGPIIAVQVENEYGSYNKDPA YMPYVKKA LEDRGIV ELLT SDNK DGLSKGIVQGV LAT
INLQSTHELQ LTTFLNVQGTQPKMVMEYWTGFDSWGPHNILD SSEV LKT VSAI VDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVT SYDYDAVLTEAGDYTA KYMKLRDFFGSISGIP
LPPPPD L LPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKP INMENLPVNGGNGQSF GYI LY
TSITSSGILSGHVHD RGQVFVN TSVIGFLDYKTTKIAVPLI QGYTVLRILVENRGRV NYGEN
IDDQRKGLIGNLYLN DSPLKNFRIYSLDMKKSFFQRFGLDKWXSLP ETPTLPAFFLGSL SIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLP GPWLSSG INQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGTGGACGGTCCCAGGACC
CTGGTGAGGGTTCTACTTGGCCTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGCTCGGCCGAGGCCCGAGCACCTCATCTCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
AAGAACGCTGTCCCTGCCCTCGTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGTCGTTCGTAGTGGATAGGGTCATGACCGGTTCTCCTAGACGGGGCC
CGTCCGCTATGTGTCGGCAGCCTGCACTACTTCGGTACCGCGGGTGCTTGGGCCGAC
CGGCTTTGAAGATGCGATGGAGCGGCCCAACGCCATACAGTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGGTCTATAACTTAATGGCAGCCGGGACCTCATGCCCTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAAGGACCTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCATCCTGGTCTCGAAAACCTGAAATTCACTAAGAACCTC
AGATCCAGACTCCTGCCCGAGTGGACTCCTGGTCAAGGTCTGCTGCCAAGATATATC
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGCTCTCGTGCACTAGCTAGG
AGAAAAGATCTTGCTCTCACACAGATGGGCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GAECTATACCACTGTAGATTGGCCAGCTGACAACATGACCAAAATCTTACCCCTGCTT
CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATT
CTGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTCCTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCACACCTAACGTTTGCTCTCGAGATGTCATCAGCAAGT
TCCAGGAAGTCCCTTGGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGGTTGGCATTACTGGCTTCTAGACTTGCTTGGCCCCGTGGGCCAT
TCATTCAATCTTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTTATGTTGTACC
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGGTGCCAATAATGGAGTC
CATGACCGTGCCTATGTGATGGATGGGTGTTCCAGGGTGGAGCGAAATATGAG
AGACAAACTATTTTGACGGGAAACTGGGTCAAACACTGGATATCTGGTGGAGAACATGG
GGAGGCTCAGCTTGGCTAACAGCAGTGACTCAAGGGCTGTGAAGCCACCAATTCTG
GGCAAACAACTTACCCAGTGGATGATGTTCCCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCTCCAGTTGCCAAATGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT
ACTCCAAACATTCCAATTTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGTTAACCTGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCCTACGTGCCAAGATTCTGCTTCTAGGGAGCCCTAACAAATT
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAACGCTAACATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATCAATTCCCTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGCACTTAAAGGTAGGCCGGCATGGTGGCTCATGC
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTAGGACTTCAAGA
CCAGCCTGGCCAACATGGTAAACCCCCGTCTCCACTAAAAAATACAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAACCTCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLLPQADTRSFVVDRGHDRFLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLHYHNGGNIISIQVE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRSAVTKGLENMLKGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVLGPLPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSATLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTG
ACCCACAATATGGCTTACATGTTAAAAAGCTTCTCATCAGTTACATATCCATTATTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACTTGAAGGAATATT
CTTCGAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAACGATTT
GCGTTCCCTCTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGAGTTAGTGAAAATAAACTTAGGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGGTGCCGATGCTGCTTGCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAATTCTGCTAACGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGTATTGCTAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACTGGAT
TTAAAGTCCAATAACATTGCAACATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT
GACTTGTAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTCTATTACCCATGTCA
AAAACCTGGAGTCACTTATTTCTCTAACACAAGCTCGAACCTTACAGTGGCAGTATT
AGTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTGATAACCCTGCCACTCGAACGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTAGGGTTAAAGTCATTCAACATTGCTTAAATTGTTGTAACCTGGAT
AAAGGGAAGGAAAATTATAATCACTAATCTGGTTCTTTAAATTGTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTGCCGTCAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRLQHISRNAQDKQELHLFMLSG
VPDAVFDTLDVLKLELIPEAKIPAKISQMNTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESLRELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS
NNIRTIEIIISFQHLKRLTCLKLWHNKIVTISSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSPLP
EKVGQLSQLTQLELKGNCLDRPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCACCGCGTCCGGCCTTCTCTGACTTGCATTTCATTCCTTTCATGACAAACTGACTTTTTATTCT
TTTTTTCCATCTCTGGGCCAGCTGGGATCCTAGGCCCTGGGAAGACATTGTGTTTACACATAAGGAT
CTGTGTTGGGGTTCTTCTCTCCCTGACATTGGCATTGCTTAGTGGTGTGGGGAGGGAGACCACGTGG
GCTCAGTGCTGCTGCACTTATCTGCCTAGGTACATGAAGTCTTTGACCTCCATACAGTATTATGCCTGTC
ATCGCTGGGTATCCTGGGCCCTGCTCTGCTGATAGTGTGCTGTCTGCTTACTTCAAATACACAAC
GCGCTAAAAGCTGCAAAGAACCTGAAGCTGTGGCTGAAAAAATCACACCCAGACAAGGTGTGGGCCAAG
AACAGCCAGGCCAAACATTGCCACGGAGTCTGCTGCAGTGCTGTGAAGGATATAGAATGTGTGCC
AGTTTGATTCCCTGCCACCTTGCTGTCGACATAATGAGGGCTCTGAGTAGGAAAGGCTCCCTCTCAA
GCAGAGCCCTGAAGACTTCAATGATGTCATGAGGCCACCTGTTGTGATGTGCAGGCACAGAAGAAAGGCACAG
CTCCCCATCAGTTCATGGAAAATAACTCAGTGCCTGCTGGAACCGAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGCAACCTTCCAGGAAGGAGTTGGGGAGAGAGAACCTCACTGTGGGAATGCTGATAAACCCAGTCA
CACAGCTGCTTATTCTCACACAAATCTACCCCTGCGTGGCTGGAACTGACGTTCCCTGGAGGTGTCAGAAA
GCTGATGTAACACAGAGCCTATAAAAGCTGCGGCCTTAAGGCTGCCAGGCCCTGCCAAAATGGAGCTGTA
AGAAGGCTCATGCCATTGACCCCTTTAATTCTCTCTGTTGGCGGAGCTGACAATGGCGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC
AGTGAGAACTGCACTGGACAATAGAAAGACCAGAAAACAAAGCATCAGAATTATCTTTCTATGTCAGCTT
GATCCAGATGGAAGCTGTGAAAGTCAAAGATTAAAGTCTTGACGGAACCTCCAGCAATGGCCTCTGCTAGGG
CAAGTCTGAGTAAAACGACTATGTTCTGTATTGAAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAACTGTTCTTCTACTACTTCTCTCCTAACATCTCTATTCCAAACTGTT
GGCGTTACCTGATACCTTGGAGGATCCTCACCAGCCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT
TGTGTGTCACATACAAGTGGAGAAAGATTACAAGATAAAACTTCAAAGAGATTTCCTAGAAATAGAC
AAACAGTGCAAATTGATTTCTGCCATCTATGATGGCCCTCCACCAACTCTGGCTGATGGACAAGTCTGT
GGCGTGTGACTCCCACCTTCGAATCGTCAACTCTGACTGTCGTGTTCTACAGATTATGCCAATTCT
TACCGGGATTCTGCTTCTACACCTCAATTATGAGAAAACATCAACACTACATCTTAACTTGCTCTTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTAAACTCTAAATGGGATAACTTGCAACTAAAA
GACCCAACTTGCAAGACCAAAATTATCAAATGTTGGAATTCTGCTCCTTTAATGGATGTTGACATCAGA
AAGGTTAGAAGATCAGTCAATTACTACACCAATAATCACCTTCTGATCCTCAACTCTGAAGTGTACACC
CGTCAGAAACAACCTCAGATTGAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATAACAA
GAAGATGATGTAATACAAAGTCAAATGCACTGGGAAATATAACACCCAGCATGGCTCTTTGAAATCCAATTCA
TTGAAAGACTATACTTGAAATCACCATTATGAGGATTTGAACTCTTGTCAAGTGTGAC
ACCTCAGATCCAATTGGGTGTTCTGATACTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTTGAGATGAAACTTGTAAAGGTGTATCCCTTATTGGACACTATGGGAGA
TTCCAGTTTAATGCCCTAAATTCTTGAGAAACTATGAGCTGTTGATCTGCAGTGTAAAGTTGATATGTGAT
AGCAGTGACCACCACTCGCTGCAATCAAGGTTGTCAGGAGACATTCTTCATATAATGG
AAAACAGATTCCATCATAGGACCCATCGTCTGAAAAGGGATGCAAGTGCAAGTGGCAATTAGGATTCAGCAT
GAAACACATGCGGAAGAAACTCCAAACCAGCCTTCAACAGTGTGATCTGTTTCTCATGGTTCTAGCTCTG
AATGTGGTGACTGTAGCGACAATCACAGTGAGGATTTGAAATCAACGGGAGACTACAATACAGAAGCTG
CAGAACTATTAACTAACAGGTCCAACCTAAGTGAGACATGTTCTCAGGATGCCAAGGAATGCTACCTCGT
GGCTACACATATTGAATAATGAGGAAGGGCTGAAAGTGACACACAGGCCATGTA

FIGURE 70

MELVRRLMPLLLLSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPESENCTWTI
ERPENKSIRIIFSYVQLDPDGCESENIKVFDGTSSNGPLLGVCSKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVGRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSMITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNNAFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDIIGPIRLKRDRSASGNQGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCAGGCTCGCGTCTCCGTTGCTGCTGTTGCTGC
TGCTGCCGCCGCCGCGCTGCCACAGCGCACGCGCTCGACCCCACCTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGCTGGTTGACCAGGCCAAGTCCGGCATCTTCATCACTG
GGGAGTGTTCGCTGCCAGCTCGGTAGCGAGTGGTCTGGTGGTATTGGCAAAGGAAA
AGATACCGAAGTATGTGAATTATGAAAGATAATTACCCCTAGTTCAAATATGAAGAT
TTTGGACCACTATTACAGCAAATTTTAATGCCAACAGTGGCAGATATTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACCTCAAACATCATGAAGGCTTACCTTGTTGGGGT
CAGAATATTGCGACTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA
ATGGTTCATCCGCTTCTGAGGATGAATCCAGTTCAAGCGGAATTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGACCCGATCAAACTGGAACAGCACAGGCTTGGCCTGGTT
ATATAATGAAAGCCCAGTCGGGGCACAGTAGTCACCAATGATCCTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTCTACCGCAGTGTATCGTTATAACCCAGGACATCTTGCCA
CATAAATGGAAAATGCAATGACAATAGACAAACTGCTGGGCTATAGGAGGGAAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTAGCAACTTGTAGAGACAGTTCATGTG
GAGGAAATCTTGATGAATTGGGCCACACTAGATGGCACCATTCTGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGTCCTGGCTAAAAGTCAATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTCTAAATGGCCACATCAGGACAGCTGGCCTTGGCCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACG
GATTCTTGAGCAAAATGGCATTATGGTAGACTGCCACAGCTAACCATTCAGATGC
CGTGTAAATGGGCTGGCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACGGATAAGAAAATTATTGGCAGTTGCCCTTCCCTTTCCACTA
AATTCTTAAATTACCCATGTAACCATTAACTCTCCAGTGCACTTGCCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAAGTGGAAACTGAAAATTGTGAAGCCATATCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAATCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGTAAAATGGTGCACCTGTATAGGGCACTTACACGAATGGAG
CTTACAGGACTGGAAGTGTCTGGGTGAGTCAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTAAATACTGTATGCTTAGGCTACACTACATTATAA
GTTTTCTTCTCAATTATAAATTAAACATAAGTGTACTGTAACTTACAAACGTTTAATT
TTTAAACCTTTGGCTTTGTAATAACACTAGCTAAACATAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSCTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVVRGTVVNTDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC
TGAGGGTGTTCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCCTGGTCCAAGGCTCTTGCAGAAGAGCT
TTCCATCCAGGTGTCAAGAATTATGGGATCACCCCTGTGAGCAAAAGGCGAACCGAGC
AGCTGAATTCACAGAAGCTAAGGAGGCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGCAGCTATGGCTGGTTGGAGA
TGGATTCGTGGTCATCTAGGATTAGCCAAACCCAAAGTGTGGAAAAATGGGTGGTG
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACATCTGAT
ACTTGGACTAACTCGTCATTCCAGAAATTATCACCAACAAAGATCCATATTCAACACTCA
AACTGCAACACAAACAGAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCC
ACTCTACAATACCTGCCCTACTACTACTCCCTGCTCCAGCTTCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTCAAGAAGTTTATGGAAACTAGCACCAGTCTACAGAAAC
TGAACCATTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTGCTCTTCTTGGTGTGAGCTGGTCTGGATTTC
TATGTCAAAAGGTATGTGAAGGCTTCCCTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGA
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCC
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTT
TTACCCCTGCCCAAGCTGGGAAATCAAAAGGCCAAAGAACCAAAGAACAGTCCACCC
GGTTCTTAAGGAACTCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAAC
CCTTCTCCTTATTGTAACCCTGCTGGATCCTATCCTCCTACCTCCAAAGCTCCC
TTTCTAGCCTGGCTATGCTCTAAATAATATCCCACGGAGAAAGGAGTTTGCAAAGTG
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCAGTGGAGAACACGTATCCCACCTGACATGCT
AGAGCAAAAGAACATGGCAGAAAAGTTAGGCCCTGAAAGCCATGGAGATTCT
ACCTAATCTCTGTAAGCTAAAATAAGAACAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGG
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCT
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTT
GTTTGATATTCTAGCTTACTTCCAAACTAATTCTATTGCTGAGACTAATCTT
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACATACCTAAC
TACATTGTTACCTCTATATAACCAAAAGCACATTAAAAGGCCATTAAACAAATGTAT
GCTGCCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAAATTAA
AGCATTAGAAAATT

FIGURE 74

MARCFSLVLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNSPKCGKNGVGVLIWKVPVRQF
AAVCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVSPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGTATTGGTGCACGACTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTCGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGTCTGCCAACCCACGGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTGGATTGTGGAGTTCTTGCAA
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGAGGGATGTTGGACGCTACTGATGTTAGTACGCCGTAC
AAAGTGAGCACATCACCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGGCAA
GGAGGCAATGCCGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTCTG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTTCAACCCCCACCACAGTGTCA
TGGGAAAACAAGAAGGATAAATAAGATCCTCATTGGCAGTGCTTCTCCTGTCAATT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG
CTGNGACTGGNTGGGCAGCATGCAGCTTGATTTAAAGAGGCATCTAGGGATTGTCAG
GCACCCTACAGGAAGGCCTGCCATGCTGTGGCAACTGTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTACTGCTTATC
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTTCTTAG
TTGACCTGCACAGCTGGTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCACCAAGGACTCTGCTTCTTAAGCCCTCTGGCTTATGGTC
TTCATTAAAAGTATAAGCCTAACTTGTGCTAGCCTAAGGAGAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAAACCCCTATTTGTGGGATTGAGAAGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGGTAGGACTTGGAGGAGAAATCCCCTGGACTTCAC
TAACCCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSPRLSRWLAQPYYLLSALLSAAFLLVRKLPPCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFKGVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRACKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGCCGCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGGACGTTGCCCTGG
GGGCCAGCCTGGCCGGTCACCCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCA
TTGCTCTGCTGCCCGGCTCCTACGGACTGCCCTCTACAACGGCTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCCTGTTACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGCGTGTGCGTGTCAAATGGTGAAGCT
GTCGGAGAACGGGCCAGAGAAGGACGTGCTGGTGGCATCGGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTCGGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGCTGG
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGCTTCCCTTACCAAGTCCCCA
ACGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCCGTG
GTGGCCTCTTGAGCAGCTTTCCGGGCTGGGAGGAGGGCCTGGACTGGTGCACCGCGGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCCGTGG
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCGCTGCACCGCTATGAT
GTATTCTGCTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAAGCT
GACGCTGACAGAGGAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC
AGCTTTGCCGCTGGAAGTCCATGGCCTGGACCGCTGCAGCCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCGTGGTCACCCGATCCTAACTGTGGGCCAGAGCCTGG
CCGAAGCTTGCGCTCCCGACCCGAGAGCCGCTTGTACGGTGTACTGCTACCGCCAGC
ACTAGGACCTGGGCCCTCCCTGCCGATTCCACTGGCTGTGTATTATTGAGTGGTT
CGTTTCCCTGTGGGTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT
TTAACATTTTTACTATTTTGAAAGCAAACAGAACCCATGCCCTCCCTTGCTCCTG
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGCCATTGCGGTTTGCGGCTCTG
GAGGGTCCCCGCCATCCAGGCTGGTCTCCCTCCCTAAGGAGGTTGGCAGAGTGGC
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGGATGGTGGCACAGTTCTCCCTGCC
CAGCCTGGGGAAAGAAGAGGGCTGGGGCTCCGGAGCTGGCTTGGCCTCTCC
CACCTCTACTTCTGTGAAGGCCGTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAAACTCCCTCCCCGT
TCCCTCTCGGTTCAAAGAATCTGTTGTCATTGTTCTCCTGTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGCTATGACTGCCCTGCC
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 78

MGLLLLVPLLLLPGSYGLPYNGFYYNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPLYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGYPR
HRRLLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSDAGPHQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEFFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKDGHDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTGCCCTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGCGCGGGTGCAGGGATCCCTGACGCCCTGTCCCTGTTCTTGTCGCTCCCAG
CCTGTCGTGCGTGTGCTTGGCGCCCCCGCCTCCCCCGCGGTGCGGGGTTGCACACCGATCCTG
GGCTCGCTCGATTGCGCCAGGGCGCTCCCAGACCTAGAGGGCGCTGCCCTGGAGCAG
CGGGTCGTCTGTGCTCTCTCCCTGCGCCGCCGGGATCCGAAGGGTGCGGGCTCT
GAGGAGGTGACCGCGGGGCCTCCCGCACCCCTGCCCTGCCGATTCTCCCTCTCCCAG
GTGTGAGCAGCCTATCAGTCACC**ATGT**CCGCAGCCTGGATCCCGGCTCTGCCCTGGTGTG
TGTCTGCTGCTGCTGCCGGGCCCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG
TTTACCAAGGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC
CTCTGAGGAATTCTCTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTTCTTCACAGTAACAAAGGCAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACGG
CAATAAGATTGTAAGCAGACATTGCATTTCTGATTGATGGAAGCTTAATATTGGGCAGC
GCCGATTAAATTACAGAACATTGTTGGAAAAGTGGCTCTAATGTTGGAAATTGGAACA
GAAGGACCACATGTGGCCCTGTTCAAGCCAGTGAACATCCAAATAGAATTACTGAA
AAACTTACATCAGCAAAGATGTTGTTGCATAAAGGAAGTAGGTTCAAGGGGTA
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGGTGGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCA
AGCCTATCCCTGAAGAACCTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGCTGT
CGGAATAATGGCTTCTTCTTACACATGCCCAACTGGTTGGCACCACAAAATACGTAAA
GCCTCTGGTACAGAACGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTAACT
CAGTGAACATTGCCCTTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCCTC
ATGCTTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTCGGACATTGGTGCCAAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCAAGTTCACTGACTATAGCACCA
AAGAGAACATGTCTAGCTGTCACTAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT
GATGCCATTCTTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCACTATCTCTGTTGGTGTGGCTTGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACGAAGGAGTCTCACGCTTCTTACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGAGAGATTCTTAGAATCCCAGCA**AT**
AATGGTAACATTGACAACAGAAAGAAAAAGTACAAGGGGATCCAGTGTAAATTGTATT
CTCATAACTGAAATGCTTCTGCTACTAGCATACTAGAACATACAAAACATTAAAGTATGTCAAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCCTCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTTCAAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTCTAACCATGCCTACTAAATGTACAGATATGCAA
TTCCATAGCTCAATAAAAGAACATTGATACTTAGACCAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATQAVSTAHPPTGKRLKKTPEKKTGNKDCDKADIAFLIDGSFNIQQRRLNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNKFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNNGFFSYHMPNWFGETKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGCTCCGCACCCGGCCCCACCGCGCCGCTCCGCATCTGCACCCGAGCCC
GGCAGGCTCCGGCGGGAGCAGACAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG
GGGCGGCGGCTGCGGGCGCAGAGCGGAGATGAGCAGCGCTGGGGCACCCCTGCTGCCTGC
TGCTGGCGGGCGGCTCCCCACGGCCCCCGCGCCGCTCGACGGCGACCTCGGCTCCAGTC
AAGCCCGGCCGGCTCTCAGCTACCCGAGGAGGAGGCCACCCCTCAATGAGATGTTCCGC
GGTTGAGGAAGTGTAGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTAACCTCCCAGCTAT
CACAATGAGACCAACACAGACAGAAGGTTGAAATAATACCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTCATCATCGACGAGGACTGTGGGCCAGC
ATGTAAGTGCAGTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGAGCTGTGTCTGGGTCACTGCACCAAAA
TGGCCACCAGGGGCAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCTCCAGAGAGGGCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA
GCTTGCCATGACCCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGACCTGATG
GAGCCTTGGACCGATGCCCTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTCGTGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTCATGGAGGAGGTGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGTGCCGGCT
GCACGTGCTGGAGGGGAAGAGATTAGATCTGGACCGAGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTTCCCAGGTGTGCTTACGGCTGGCTGACCGAGGCTTCTTCTACA
TCTTCTTCCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTTCA
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGCTTGGGAGAGTCAGGCAGGGTTAAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACCAAGTTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAACATCAA
CCTGGAAAAATGCAACAAATGAATTTCACGCAGTTCTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTCACCCCTGCATTACATGTGTTATTCA
AGCAGTGTGCTCAGCTCCTACCTCTGGCCAGGGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGGAGGGGTCAATTGTTCTCTCGTCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACAGCAGAGCAGTT
CTGGTTGTGACTCTAACGTCAGTGCTCTCCACTACCCACACCCAGCCTGGTGCCACCAA
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTCTTGAGGCATGCACATCTGGAATTAAAG
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCCGTCTTCTAACGACAATGATATTGACACTGTCCCTTTGGCAGT
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATACTGGTAAACCTGCAGAAACA
GTACTTAGTAATTGTAGGGCGAGGATTATAAAATGAAATTGCAAACATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTCACTCCAGAGTTCTAAAGTTAAAGTTGACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTTAAACATAAGTTGACATTAGAAATCAAGC
ATAAAATCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLANLPPSYHNETNTDKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECI IDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCQAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRPCASGLLCQPHSHSLVYVCKPTFGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGAAAGAGGTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTTCAGCCCCATCCACTCTCCCTCCAAACACACATGTGCATGTACACACACATACA
CACACATACACCTTCTCCCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCAAGAAAAGGACAC
TAAAGCCTTAAGGCAGGCCATTACCTCTGCAGCTCTGGTTGAGTCAAAAAAACATGGGAGGGG
CCAGGCACGGTCACTCACACCTGTAATCCCAGCATTTGGAGACCGAGGTGAGCAGATCACTTGAGGTCAAGGAG
TTCGAGACCAGCCTGCCAACATGGAGAAACCCCCATCTACTAAAAAATACAAAAAATTAGCCAGGAGTGGTGGC
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAATCGCTGAACTCAGGAGGCGAGGATGCAGT
CAGCTGAGTGCACCGCTGCACTCCAGGCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACACGGGAGGA
GGGGTAGATACTGCTCTGCAACCTCTTAACCTGCATCCTCTTCCAGGGCTGCCCTGATGGGCCTG
GCAATGACTGAGCAGGCCAGGCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGA
GCCCCCGTGTGAGCTGGCTGGGGTGGTCCCTGGGCCCTGGCAGGGTTGCTGACCCCTAACCTGCAAAACACA
AAGAGCAGGACTCCAGACTCTCCTGTGAATGGTCCCCCTGCCCTGAGCTCCACCATGAGGTTCTCGTGGCCCC
ACTCTGCTAGCTTGGGTGGCTGGCCACTGCCACTGTGCCGTGGTACCCCTGGCATGTTCCCTGCCCTCTCA
GTGTGCCTGCCAGATCGGGCCCTGGTATACGCCCGCTGCTTACCGCAGGGTACCAACTGTGGACTGCAATGA
CCTATTCCCTGACGCCAGTCCCCCGGCCACTCCCCGAGGACACAGACCCCTGCTCTGCAGAGCAACAGCATTGT
CCGTGTGGACCAGAGTGAGCTGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCAGAACAGCTTTCGGA
TGCCCCAGACTGTGATTCCATGCCCTGCCAGCTGCTGAGCCTGCACCTAGAGGAGAACAGCTGACCCGGCT
GGAGGACCACAGCTTGCAAGGCTGGCCAGCCTACAGGAACCTATCTCAACCACAAACAGCTTACCGCATTG
CCCCAGGGCTTTCTGCCCTCAGCAACTTGCTGCGCTGACCTCAACTCCAACCTCTGAGGGCATTGACAG
CCGCTGGTTGAATGCTGCCAACCTGGTAGCCTGGTCTAGCAGGCATGAACCTGCCGGAGATCTCGACTATGC
GAACCTCCGGCCCCCTGCCAACCTGCGTAGCCTGGTCTAGCAGGCATGAACCTGCCGGAGATCTCGACTATGC
CCTGGAGGGCTGCAAAGCTGGAGAGCCTCTCTATGACAACCCAGCTGGCCGGGTGCCAGGCCGGCACT
GGAACAGGTGCCGGCTCAAGTCTTAGACCTCAACAAGAACCCGCTCCAGCAGGGTAGGGCGGGGACTTGC
CAACATGCTGCACTTAAGGAGCTGGGACTGAACAAACATGGAGGAGCTGGTCTCATGACAAGTTGCCCTGGT
GAACCTCCGGAGCTGCCAACAGCTGGACATCACAATAACCCACGGCTGTCTCATCCACCCCCGGCTTCCA
CCACCTGCCCGAGATGGAGACCCCTCATGCTCAACAACACGCTCTCAGTCCCTTGACCCAGCAGGGTGGAGTC
CCTGCCCAACCTGCAAGGAGGTAGGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTCATCCGCTGGGCAATGC
CACGGGCAACCGTGTCCGCTCATGAGCCGAATCCACCCCTGTGTGCGGAGCCTCCAGCGCTTCC
GGTCCGTGAGGTGCCCTCCGGAGATGACGGACCACGTGTTGCCCTCATCTCCCCACGAAGCTCCCCAAG
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCAATTGCCGGCACTGCCGAACCCGAACCGAGATCTACTG
GGTCACTCCAGCTGGCTTCGACTGACACCTGCCATGCAAGGAGGTACCGGGTGTACCCGAGGGGACCC
GGAGCTGGAGGGTGAAGCAGCAGAAGAGGAGGGCTATACACCTGTGTGCCCAGAACCTGGTGGGGCTGACAC
TAAGACGGTTAGTGTGGTGTGGCCGTCTCCCTCAGGCCAGGAGCAGGGAGCAAGGACAGGGCTGGAGCTCCG
GGTGCAGGAGACCCACCCCTACACATCCTGCTATCTGGTCAACCAACAGTGTCCACCAACCTCAC
CTGGTCCAGTGCCTCCCTCCGGGCCAGGGGCCACAGCTCTGGCCGCTGCCTGGGAACCCACAGCTA
CAACATTACCCGCTCCTTCAGGCCACGGAGTACTGGCCTGCTGCAAGTGGCTTGTGATGCCACACACCA
GTTGGCTTGTGATGGGCCAGGACAAAGAGGCCACTCTTGTGCAAGAGCCTTACGGGATCGTCTGGCTCAT
TGCCATCCTGGCTCTGCTGTCCTCTGGCAGCTGGTCTAGCGGGCACCTGGCACAGGCCAACCCAGGAA
GGGTGTGGTGGGAGGCGGCCCTCCCTCCAGCTGGCTTCTGGGCTGGAGTGGCCCTTCTGTCCGGTTGT
GTCTGCTCCCTCGCTGCCCTGGAAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC
ACCATTGTCTAAAAATTCTGAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTACCAAA
AGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGGAAAGGGACATGGACCCACGTGCTTGAGGGCTGGCAGTGGC
CAAGACAGATGGGGCTTTGTGGCCCTGGGCTGCTCTGCAGCCTGAAAAAGTTGCCCTAACCTCCTAGGGTCA
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGGAGGGACTTGGCTAGAGCCTCTGCCCTCCCATCTT
CTCTCTGCCAGAGGCTCTGGCCTGGCTTGTGCTTACCTGTGTCCTGGGCTGCAACCCCTTCTCTTC
TCTTCTCTGTACAGTCTCAGTTGCTGCTCTGTGCTGCCCTGGCAAGGGCTGAAGGAGGCCACTCCATCTCAC
CTCGGGGGCTGCCCTCAATGTGGAGTGAACCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAA
CGCCTCATCTCAGCAGCCTGGCTGGCATTCCAAGCTGACTTTCTATAGGCAATTGTACCTTGTGGAGAA
ATGTGTACCTCCCCAACCGATTCACTCTTCTCTGTAAAAATAAAATAACAATAAAA
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTLDLSQNSFSDARCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANRSLVLAGMNLR EISDYALEGLQSLSFYDNO
LARVPRRALEQVPGLKFLDLNKNPLQRVPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHHLQPMETLMLNNNALSAHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPLSQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGADTKTVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACIQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALA VLLAAGLA AHLGTGQPRKGVGRRPLPPAWAFWGWSAPS VRVV
SAPIVLPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGCCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGGGGACATTGTGTACCGCCT
CTACATCGGGCAGACCCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCAACCC
CCTGCCAACACTCTCAAGATCCTGGCGCTCTTCTACATCAGCCTAGTCATCTTACCGCCTCATCTGCATGTA
CACACATGTGGTGGATGCTACGGCGTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCTCATGCTGCACCTCATGACCAATACGACCCGCTCTACTCCAA
GCGCTTCGCCGCTTCTCTCGAGGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCC
CAGCATTGCCAGCTCACGGGCTCAAGGAGCTGTGGCTCTACCACACAGGGCAAGATTGAGCGCTGCGCT
GGCCTTCCTGCCGAGAACCTGCGGGCCTGCACATCAAGTCACCGACATCAAGGAGATCCCCTGTTGATCTA
TAGCTGAAGACACTGGAGGAGCTGCACCTGACGGCAACCTGAGCGGGAGAACAAACGCTACATGTCATCGA
CGGGCTGCCGAGCTAACGCCTCAAGGTGCTGCCGCTCAAGAGCAACCTAACGAAGCTGCCACAGGTGGTCAC
AGATGTGGCGTGCACCTGAGCTGCTCCATCAACAAATGAGGGACCAAGCTCATCGTCCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCCACCTGGAGCGCATCCCCCCTCCATCTCAGCCT
CCACAAACCTGCGAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTCCAGCACCT
GCACCGCTCACCTGCCCTAACGCTGTTAACACCACATGCCCTACATCCCCATCCAGATCGGCAACCTCACCA
CCTGGAGCGCCTCACCTGAACCGAACAGATCGAGAAGATCCCCACCCAGCTTCTACTGCCGAGCTGCG
CTACCTGGACCTCAGCCACAACAACCTGACCTTCCCTGCCACATCGGCCCTCTGCAGAACCTCCAGAACCT
AGCCATCACGGCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGCCGAGCTGACCAACCTGACGAGATCGCGGG
GGCAACAAACGTGCTGCAGTCAGTGCCTCCAGGGTGGCGAGCTGACCAACCTGACGAGATCGCGGG
CAACCGGCTGGAGTGCCTGCCGTGGAGCTGGCGAGTGCCTCAAGCGCAGCGGCTTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCTTAG
GCCGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGAGGGCAGGCTAGCTTCTCCAG
AACTCCCGACAGCCAGGACAGCCTGCCGTGGCAGGAGCCTGGGCCGTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGCTGCCCTTCTCCCTTGAGACTCACGCCCCAGGGCAAGTGCTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTGATAATCAGGGTCTCTCCCTGGAGGCCAGCTCTGCCCTAGGGCTGAG
CTGCCACAGAGGTCTGGGACCTCACTTTAGTTCTGGTATTATTATTTCTCATCTCCACCTCCTCATCC
AGATAACTTATACTTCCCAAGAAAGTTGAGCCAGATGGAAGGTGTTCAAGGGAAAGGTGGCTGCCCTTCCCC
TTGTCCTTATTAGGATGCCGGGGCATTAAACACCCACCTGGACTTCAGCAGACTGGTCCGGGGCAACCCAG
CCATGGGACGGTCACTGCCAGCAGTGCCTGGCTGGGCTCTGGGTGCGGTCCACGGAGAGCAGGCCCTCAGCTGGA
AAGGCCAGGCCAGTGGAGCTTGCCTCTTCACTTTAGTTGTGGAGTTAGTTTTTTTTTTTTAAATCAA
AAACAATTTTTAAAAAAAGCTTTGAAAATGGATGGTTGGTATTAAAAAGAAAAAAACTTAAAAAA
AAAAGACACTAACGGCCAGTGGAGTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAGCAGCAGACGT
TGAACGTGTTCTTCCCTGGGAGGGAGTTTTTGTGTTGGTTTTGGGTTTTTGTGTTCTGTTCTTCTCCTCC
CTATTGTTCTGGGAGGGACTCATTTCTGTTGCTGCGGCCAGAGGGAAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTGGCTAATCCCCGGATGAAACGGTGTCCATTGCACCTCCCTCTGCGCTGCCCTGCCCTCTCCA
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTCGCCCAGACTTTGTTCCCCACCTCTGCCATGGGTGTT
CCAGTGCACCGCTGCCCTCCGCTGCTCCATCAGCCCTGCGCACCTGGCCTTCTGAGACACTTA
GAGGCTGGTCGGAATGGGGAGGTGCGCCCTGGAGGGCAGGGCGTTGTTCAAGCCGGTCCCGTCCGGC
CTGGAGTGACACAGCCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTAGATCACTCGGGTCCCCACCT
AGAAGGGTCCCCGCCCTAGATCAATCACGTGGACACTAAGGCACGTTTAGAGTCCTTGTCTTAATGATTATGT
CCATCCGTCTGTCGTCCATTGTTCTGCGTCGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATAA
ATCTATAACAGAAAAAA

FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIFDVDCVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNLNNEWTLDKLQRQLTKNAQDKLELHLFMLSGLPDTVFDLVELEV
LKLELIPDVТИPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSQLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCCGTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAATTGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGCACTGGGTTAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCAGAGCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCACATCAAGTGCAACTTGCGGGGGT
TGCCTGGGTGATTCTGGATCTCCCTGGTGAAGACCTTCTCAGTTGCCACAAAG
ACAGCATGTCTCTCGAACAGACAAAGGTCTGGCAGAGGTGTCAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTTCTATAACATCTTAACACTAAAGCACTCCA
CGTCTACAATGGAGTCGAGTCAGATTACACAGAGCCACCTAGTTGTCTTGTCAAGGC
CACGTGAGACACCTACAACGAGATGCCCTAACGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTAAAATTATTCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATAACATGGGTCAAGGAGGC
GGTGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCC
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTGAUTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGC
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGAGAGGATAAAACATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTTCTTAAAAACCTAAGATTTTAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEWWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELGKAEMIIEQNTDGVNFYNLTKSTPTSTMESLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQOE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCCGCGCCGTATCAGGACCATGCGGCCGA
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGGACGCCGA~~CT~~CGGCCGTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCCGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGCGCACTGCTTGAAACCTATA~~G~~TGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGCCAGCTGACTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTACCCTATGACATTG
CCTTGGTGAAGCTGTCACCTGTCACCTACACTAAACACATCCAGCCC~~AT~~CTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTACTGGCTGGGTACATCAA
AGAGGATGAGGC~~ACT~~GCCATCTCCCCACACCCTCCAGGAAGTT~~CAGG~~TGCCATATAAACAA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGT~~TT~~CCGAAGGACATCTTGAGACATG
GTTTGTGCTGGCAACGCCAAGGCGGGAGGATGCC~~T~~GCTGCTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTCTACACCAATATGCCACCACTT~~G~~AGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTTGAGCCTACCTGAGCC~~AT~~GCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTGTCTTGTAA~~AA~~ACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCGVSLLSHRWALTAAHCFETYSIDLSDPSGMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEJVQAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWVGCGRPNRPGVYTNISHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACCGCGTCCGCGGACCGGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCCGAGGCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGTCCTGGCCGTGCGGACCCCTGAGGAAGAGCTGAGTCTCACCTT
GCCCTGAGACAGCAGAAATGTGAAAGACTCTCGAGCTGGTGCAGGCTGTGTCGGATCCCAG
CTCTCCTCAATAACGAAAATACCTGACCCCTAGAGAATGTGGCTGATCTGGTAGGCCATCCC
CACTGACCCCTCCACACGGTGAAAAATGGCTCTTGGCAGCCGGAGCCCAGAAGTGCCATTCT
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTCCACAGGCCTGGCCCCCATGTGGACTTTGTGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGCAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCCCTGTGATCCGTAAGCGATAACAACCTGACCTACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTTCATGCGCCTCTCGGTGGCAACCTTGACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGGCCGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGTGGTGCACATCTCACCTGGGCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCCTACATCCAGCAGGTCA
ACACTGAGCTCATGAAGGCTGCCCTGGGCTCACCCTGCTCTGCCCTCAGGTGACAGT
GGGGCCGGGTGTTGGCTGTCTGGAAAGACACCAGTTCCGCCCTACCTTCCCTGCCCTCCAG
CCCCTATGTCACCACAGTGGGAGGCACATCCTCCAGGAACCTTCCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCATG
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTCTGATGGCTACTGGTGGTCAGCAACA
GAGTGCCCATTCATGGGTGTCGGAACCTCGGCTCTACTCCAGTGTGTTGGGGGATCCTA
TCCTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCTCTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGGATCTGTAACAGGC
TGGGGAACACCAACTTCCAGCCTTGCTAAGACTCTACTCAACCCCTGACCCCTTCTATC
AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTATTCTGCCCTGTT
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCGTAAA
TGCTGTGAGCTTGACTTCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGAAATGCCCTCTCCCTCCGC
ATCTCATCTTCTCTTCAATCAGGTTTCAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTGATATTCAATTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT
TTCCTACCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTGCTTTATG
GCCTTCCATCATAGTTGCCACTCCCTCTCCTACTTAGCTCCAGGTCTTAACCTCTG
ACTACTCTTGTCTCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTGC
TCCATTGTAGATTTGCTCTCAGTTACTCATTGCCCCCTGGAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATAACCTCAAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGHLRFPPSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLFASGDGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHECLDEEVEGQGFCSGPWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGCGCGCGCTCTCTCCC GGCGCCACACCTGTCTGAGCGCGCAGCGAGCCGGCCGGC
GGGCTGCTCGCGCGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTTCTC
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATAACGCCCTCCCTGTCGCTTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTCAAGGAACT
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAGGACTTCCTGCTCAACTACCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCCCTGGTGGCAGAGAAGCATGTCCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCAGCCATGCCGAGCAGATGAA
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA
ATTCAGTGGATCCGGTGAAACGCACCCATGTGCCAAGGGTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGAACTCAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCTGCTAACGCAGCTGCCAGGGGCCAGGGTCTGGGTCTAT
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCTCTACCAGCAATGCGATGCCAGCCAGGGGCCAGGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAATTATTGGCTTTTCAGG
GCACCAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGTCCCTGGCAGCAATTAGGGCTTCATGTTCTTATTAGGAGAGGCC
AAATTGTTTGTCTGGCGTGCACACGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAATG
GTTTGTGTATCATATCATATCATTTAACGAGCTTGAAGGCATACTTTGCATAGAAATAA
AAAAAATACTGATTGGGGCAATGAGGAATATTGACAATTAGTTAATCTCACGTTTGT
CAAACTTGATTTATTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLQPSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIVIYLSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTA
AHCIDHGKTYVK
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMFKFWIRVKRTHVPKGWIKGN
ANDIGMDYDYA
LLELKPKHDKFMKIGVSPPAKQLPGGRIHFGSYDNDRPGNLVYRFCDV
KDETYDLLYQQCD
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNV
AVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCCAGCCTGGGTGGGGCTGTCTCGGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGCGGCCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTGCTCACCAAGCCGTGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATAACCTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCTGGCTCTCGTCCCAGAAGGTGGTGTTGCCCTGGTGGAGC
CCCACCCCTGTGTATT CCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCCTCAGACCCCTGCAGAACGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTGTCTGGCGACTCCGGGGCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCGGCATCATCAGCTGGGGAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAACATCGTCAAGGGGTGCA
GCTCCCGGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCCG
CCGCGCGCTCCTAGGGCGCAGCGGGACGGGGCTCGGATCTGAAAGGCGCCAGATCCACA
TCTGGATCTGGATCTGGCGGGCTCGGCGGTTCCCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCTCCAAGGCATCAGGCCGCCAACGGCCTCATGTCCCCGCCAAC
GACTTCGGCCCCGCCCGGGCCCCAGCGCTTTGTATATAATGTTAATGATTTTAT
AGGTATTTGTAACCCTGCCACATATCTTATTATTCTCCAATTCAATAAATTATTATT
CTCCAAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFVLLGAWQLGNPGSRSQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC
QVDGAWLLAGIIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSGQ
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTGATGCTTCGTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTCGCCAAGGCCCTACGCACGGCAGTGCCTGTGGGCCAC
AACAAAGGAGCGCGGGCGCCGCGCGAGAAATCTGTCGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAAACCTCAGGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC
GGCTGTGGTCCCACCTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTTGCCCTACCTGGTAAC TGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCCCTAGCAACGGGATTCCGGCTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCGCCTGCTGTGGAAACCCAGGCC
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTT CCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCTGACAGGGCAAG
GGAACCTCCTACCCATGCCAGGAGGAGGCTGAGGCTGAGTTGCCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCAAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCGCAGTCCTGCCAGGTGAGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGTATGTTGGGGCCCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGATCTTCTTGAATGGGATACCAACTCAAAGGG
TGAAGAGGT CAGCTGTCCTCCTGT CATCTTCCCCACCCCTGTCCCCAGGCCCTAAACAAAGATA
CTTCTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGCATGTGCCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCTCCCTGGTGGCTGGAGTCCTGGGGTGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCCCTCCCTGAGTGCCTG
TGTAGCTGGGGATGGGATTCTAGGGCAGATGAAGGACAAGGCCCACTGGAGTGGGTTC
TTTGAGTGGGGAGGCAGGGACGGAAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVETNIELLVCNYEPPGNVKGKRPYQEGETPCSQC
PSGYHCKNSLCEPIGSPEADAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCTEVPSILAHSPLSDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENS LPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTAGGCTTCAATTGGAGCCCTCAACAGAACCGTCATTCTCCAAGTTATGGTGGACGT
ACTTCTGTTCTCCCTCGCTTGCATTTCACATTAGCAGACCGACTAACAGATTATCTTCAT
CAAGGCAAGTCCATGAGCACCTTCAAAGCCTCGAGAAACTGAACAACAATGAATTGGAGACCATTCC
AAATCTGGGACCAGTCTGCAAATATTACACTCTCTCCGGCTGAAACAGGATTGAAACTCCCTGA
ACATCTGAAAGAGTTCAGCCCTGAAACTTGGACCTTAGCAGCAACAATATTAGCAGCTCCAAACTGCATT
TCCAGCCCTACAGCTAAATATCTGATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTGGACAA
TTTGGCCAACACAACTCCTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAAACT
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATAAAAATGTAGATGGACTGACATTCCAAGGCCCTGG
TGCTCTGAAAGTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGCTTTGGGGCTGAGCAA
CATGAAATTTGCAAGCTGGACCATAACACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGCTGATGCT
GCAGGAACATTCTCATCTCAGCCAAAATGCCATCACAGGATCAGCCCTGATGCCCTGGAGTCTGCCAGAACGCTCAG
TGAGCTGGACCTAACTTCAATCACTTACAGGTTAGATGATTCAAGCTTCTGGCCTAAGCTTAACTAAATAC
ACTGCACATTGGAAACACAGACTCAGCTACATGCTGATTGCTTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAGAACATGAAATTCCCTGGACTATTGAAGACATGAATGGTCTTCTGGGCTTGACAAACTGAG
GCGACTGATACTCCAAGGAAATGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCATTGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGCTTACAAGGCAATGCAATTTCACAAATGAAGAAACTGCAACAATT
GCATTAAATACATCAAGCCTTTGCGATTGCCAGCTAAAGGCTCCACAGTGGTGGCGAAAACAACCTT
TCAGAGCTTGTAAATGCCAGTTGCTGCCATCCTCAGCTGCTAAAGGAGAACGATTTGCTGTTAGCCAGA
TGGCTTGTGTGATGATTCCAAACCCCCAGATCACGGTTCAGCCAGAAACACAGTCGCAATAAAAGGTT
CAATTGAGTTTCATCTGCTCAGCTGCCAGCAGCAGTGAATCCCCATGACTTTGCTGGAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAAATTATGCACACCTCCGGGCCAAGGTGGCGAGGTGATGGAGTATACCAC
CATCCCTCGGCTGCGGAGGGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCCAATCACTTGGTTC
ATCCTACTCTGCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATCACCACGCCCCATGGATCTCACC
CCGAGCTGGGGCATGGCACGCTGGAGTGCTGCTGTGGGACCCAGCCCCAGATAGCCTGGCAGAACGGA
TGGGGCACAGACTCCAGCTGCACGGGAGAGACGCATGATGTGATGCCAGGATGACGTGTTCTTATCGT
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTCAGCAAATGC
AACTCTGACTGCTCTAGAACACCATCATTGGCGGCCACTGGGACCGAAGTGAACCAAGGGAGAAACAGC
CGTCTACAGTGCATTGCTGGAGGAAGCCCTCCCTAAACTGAACTGGACCAAGATGATAGCCCATTGGTGGT
AACCCAGAGGCACTTTTGCAAGCAGGCAATCAGCTCTGATTATTGGAACCTCAGATGTCAGTGTGATGCTGGAA
ATACACATGTGAGATGCTAACACCCCTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAAC
CTGCGACTCCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGTGTGATCATAGC
CGTGGTTGCTGTGGTGGCACGTCACTCGTGTGGTGTGATCATACACACAAAGGGAGGAATGAAGA
TTGCACTTACCAACACAGATGAGACCAACTTGCAGCAGATATTCTAGTTATTGTCATCTCAGGGAACGTT
AGCTGACAGGCAGGATGGTACGTGCTTCAGAAAGTGGAGCCACCCAGTTGTCACATCTCAGGTGCTGG
ATTTTCTTACACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAGCTGC
CACAGATCTGTTCTTGTCCGTTGGATCCACAGGCCCTATGATGTTAGGAAATGTGATGCTCAGA
TCCTTTGAAACATATCATACAGGTTGCAGTCTGACCCAGAACAGTTTAAAGGACACTATGAGCCAGTT
CATAAAGAAAAAGGAGTGTACCCATGTTCTCATCCTCAGAAGAACCTGCGAACGGAGCTCAGTAATATATC
GTGGCCTTCACATGTGAGGAAGCTACTTAACACTAGTTACTCTCACAAATGAAGGACCTGGAATGAAAATCTGT
TCTAAACAAGTCTCTTGTAGATTAGTGCACATCCAGGCCAGCGTCGGTGCCTCGAGTAATTCTTCATGG
TACCTTGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAGCC
AAGAGCCTTTATTGAAAGCTCATTCTCCAGACTTGACTCTGGGTGAGGAAAGATGGAAAGAAGGAC
AGATTTCAGGAAGAAAATCACATTGTACCTTAAACAGACTTTAGAAAACAGTCCAAATTTCAGTC
TTATGACTGGACACATAGACTGAATGAGACCAAGGAAAGCTTAAACATACTACCTCAAGTGAACCTTTATT
AAAGAGAGAGAATCTTATGTTAAATGGAGTTATGAATTAAAGGATAAAAATGCTTATTATACAGAT
GAACCAAATTACAAAAGTTATGAAATTTTAAACTGGGAATGATGCTCATATAAGAACACCTTTAAACTA
TTTTTAAACTTGTGTTATGCAAAAAGTATCTACGTAATTAAATGATATAAATCATGATTATTGATTT
TTATAATGCCAGATTCTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCACTTT
TTAAATAGAAGTTACTTCATTATATTGCACTTAAATGTCATTTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRDPDLSHNRLSIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLVLKLNRRNRIASIPPKMFKLPQLQHLELRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMGDGFWGILSNMEIILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE
FCQKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWLPOWVAENNFSFVNASCAPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSI SANATLTVLETPSFLRPLLDRVTKGAVLQCIAGGSPPKLNWTKDDSPVTER
HFFAAGNQLLIIVDSDVSDAGKYTCMSNTLGTERGNVRLSVIPTPTCDSPQMTAPS LDDDG
WATGVVIIAVVCCVVGTSLVWVVIYHTRRNEDCSITNTDETNL PADIPS YLSSQGT LAD
RQDGYSSES GSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDPFETYHTGCSPDPRTVLMHYEPSYIKKKECYPCHPSEES CERSFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENY RTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGAAAAGGAGACTTTTTGGTGGTGGCTGTTGGGTGCCTTGCAAAATG
AAGGATGCAGGACGCAGCTTCCTGGAACCGAACGCAATGGATAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTGTGAGCCTGGATCTAACACAATGTGTATATGTGACACAGGGAGCATCAAGAATGAAA
TAAACCAGAGTTAGACCCGGGGGGTTGGTGTCTGACATAAATAATCTAACAGCTGTTCCCCTCC
CCACCCCCAAAAAAAGGATGATTGGAAATGAAGAACGAGGATTCAAAAGAAAAAGTATGTCATTTCCTC
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTTGGAAATGAAAAGTGGGGCTTTTAGTAAAGTAAGAAACT
GGTGTGGTGGTCTTCTTCTTGTAAATTCCCACAAAGGGAGAGGAAATTAATAATCATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTTGACCGCGCACATTGAGGCATTGAGGATTGGGGAGAGAACGAGCACAGTTGGA
TTTGTGCCATGTTGACTAAAATGACGGATAATTGCAAGTGGATTCTTCATCAACCTCCTTTTTAAAT
TTTATTCCCTTGGTATCAAGATCATGCGTTCTCTTGTCTTAACACCTGGATTCCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACGTGTTGAATTCCAGAACGGACCAACACAGATAAAATTATGAATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTAACAGGGCCCTATTGACCCCTGCTGTGGTGC
GCTGGCTCTTCAACTCTTGTGGTGGTCTGGTGGCTCAGACCTGCCCTCTGTGCTCTGAGCAA
CCAGTTCAGCAAGGTGATTGTGTTGGAAAAACCTCGCTGAGGTTCCGGATGGCATCTCCACCAACACGGCT
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCAGTGAGGACTTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCAATTGAATTGGGGCTTCAATGGTCTGGGAACCTCAACACTCTGGA
ACTCTTGACAATCGTCTTACTACCATCCGAATGGAGCTTGTATACTTGTCTAAACTGAAGGAGCTCTGGTT
GCGAAACAACCCATTGAAAGCATCCCTTCTTATGCTTTAACAGAACCTCTTGCCTGGACTAGACTTAGG
GGAATTGAAAAGACTTTCATACATCTCAGAACGGCCCTTGAAGGTCGTCCAACCTGAGGTTTGAACCTTG
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAACAGATGAGCTGGATTTCTGGGAATCA
TTTATCTGCCATCAGGCCTGGCTCTTCAGGGTTGATGCACCTCAAAACTGTGGATGATACTGCCCAGAT
TCAAGTGATTGAAACGGAATGCCCTTGACAACCTCAGTCACTAGTGGAGATCAACCTGGCACACAATACTAAC
ATTACTGCCTCATGACCTCTTCACTCCCTTGACATCATCTAGAGCGGATACATTACATCACACCCCTGGAACTG
TAACGTGACATACTGTGGCTCAGCTGGATAAAAGACATGGCCCTCGAACACAGCTTGTGCTGCCGGTG
TAACACTCCTCCAATCTAAAGGGAGGTACATTGGAGAGCTGACCAGAATTACTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCTGAGCTGAAATGTCGGGCTCCACATC
CCTGACATCTGATCTGGATTACTCCAATGGAACAGTCATGACACATGGGGCTACAAAGTGCCTAGCTGT
GCTCAGTGTGATGGTACGTTAAATTCAAAATGTAACCTGTGCAAGACATAGGCATGTACACATGTATGGTGGTAA
TTCCCTTGGGAATACTACTGTCTCAGGCCACCTCTGAATGTTACTGTCAGCAACACTACTCCTTCTTACTTT
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGGACACAGATAACAAATGTGGGTCCCAC
AGTGGTCGACTGGGAGACCAATGTGACCACCTCTCACACCCACAGAGCACAGGTCGACAGAGAAAACCTT
CACCATCCCAGTGAACATGATATAAACAGTGGGATCCAGGAATTGATGAGGTCTGAAGACTACAAATCATCAT
TGGGTGTTTGTGGCCATCACACTCATGGCTCAGTGTGATGTCAGTGGTCTTCTACAAGATGAGGAAGCAGCACCA
TCGGAAAACCATCACGCCAACAGGACTGTGAAATTATTAATGTGGATGAGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCT
CAACCCACACAACACAGTTAACACAATAACAGTTCACTGTCAGTGCATGAAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAAAACAAACAATCAAAAAAA
GACAGTTTATTAAGACACAAATGACTGGCTAAATCTACTGTTCAAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAATTATTATTAAAGTGTGATCTAAAGCAGACAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNADFNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWCNCDIL
WLSWWIKDMASTSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSGTLNFTNVTVQDTGMYTCMVSNVGN
TTASATLNVTAATTTPFSYFSTVTETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDEITGDTPMESHPMPAIEHEHLHYNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACCGCTGCTCAAGCTGCAACTCTGTGCAAGTTGGCAGTTCTTTCGGTTTCCCCTCCTGCTGTTGGGGCA
TGAAAGGCCTTCGCCGCCGGAGTAAAAGAAGGAATTGACCAGCGCAGGCCAGGGAGGAGCGCCACCGAACCGC
GAGGGCAGGGCGTGCACCCCTCGGCTGGAAGTTGTGCCGGGCCCCGAGCGCGGCCGCGGGCTGGAGCTTCGGGTAGA
GACCTAGGCCGCTGGACCGCGATGAGCGGCCAGGCCCTCGTGCAGCGCCGCCGGGTTGGGCTGCTGCTGTGC
GCGGTGCTGGGGCGCGTGGCCGGTCCGACAGGGGGACTCGGGGAGCTCGGACTGCACTGGGAGCCCTCTGGGGTAGCCGCC
GAGGCCCATGCCCACTACCTGCCCTGCCCTGGGACTGCAAGGGCTAGCGCTGTAAGCGGCTAGCGCTCTT
CCCGAGCCACTCCGCTGGACTTAAGTCACAACAGATTATCTTCATCAAGGCAAGTCC
ATGAGCCACCTCAAAGCCTCGAGAAGTGAAGACTGAACAACAATGAATTGGAGGACCAATTCCAATCTGGGACCA
GTCTGGCAAATATTACACTTCTCTGGCTGAAACAGGATTGTGAAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTGAAACTTTGGACCTTAGCAGCAACAATTTCAGAGCTCAAACGTCATTTCCAGGCCACAG
CTCAAATATCTGTATCTAACAGCAACCGAGTCACATCAATGAACTGGTATTITGACAATTGGCCAACACA
CTCCTGTGTTAAAGCTGAACAGGAACCGAATCTAGCTATCCCAAGATGTTAAACTGCCCAACTGCAAA
CATCTCGAATTGAAACGAAACAAGATTAAAATGTAGATGGACTGACATTCAAGGCCCTGGTGTGCTGAAAGTCT
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAACATGAAATTGG
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTGCTGATGCTGCAGGAACCTCAT
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAGCTCAGTGAGCTGGACCTA
ACTTCAATCACTTATCAAGGTTAGATGATTCAAGCTCCCTGGCCTAAGCTACTAAATACACTGCACATTGGG
AACACAGAGTCAGCTACATTGCTGATTGCTGCCCTCCGGGGCTTCAGTTAAAGACTTGGATCTGAAAGAAC
AATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTGGGCTTGACAAACTGAGGCGACTGATACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCACTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGTCTTACAAGGCAATGCAATTCAACAAATGAAGAAACTGCAACAATTGCAATTAAATACA
TCAAGCCTTTGTGCGATTGCCAGCTAAATGGCTCCCACAGTGGTGGCGAAAACAACCTTCAGAGCTTGTA
AATGCCAGTTGCCCCATCCTCAGCTGCTAAAGGAAGAACGATTTTGCTGTTAGCCAGATGGCTTGTGTTG
GATGATTTCACCAACCCCCAGATCACGGTTCAGGCCAGAAACACAGTCGGCAATAAAGGTTCAATTGAGTTTC
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTGCTGGAAAAAAAGACAATGAAACTACTGCATGAT
GCTGAAATGAAAATTATGCAACACCTCCGGGGCCAAGGTGGCAGGTGATGGAGTATACCACCATCTGGCTG
CGCGAGGTGGAATTGCCAGTGAGGGGAAATATCAGTGTGTCATCTCCAATCATTGGTTCATCTACTCTGTC
AAAGCCAAGCTACAGTAAATATGCTTCCCTATTCCAAGACCCCCATGGATCTCACCACCGAGCTGGGGCC
ATGGCACGCTGGAGTGTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGCACAGAC
TTCCAGCTGCAAGGGAGAGACGCATGCATGTGATGCCAGGATGACGTGTTCTTATGTGGATGTAAGATA
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAAGGATATTGCAAATGCAACTCTGACTGTC
CTAGAAACACCATATTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAACAGCCGCTCACAGTGC
ATTGCTGGAGGAAGGCCCTCCCCCTAAACTGAACTGGACCAAGAGATGATAGCCCATTGGTGTGACAGGAC
TTTTTGAGCAGGCAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGAAATACACATGTGAG
ATGCTAACACCCCTGGCACTGAGAGAGGAAACGTGCGCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCT
CAGATGACAGCCCCATCGTAGACGATGACGGATGGCCACTGTGGGTGCTGATCATAGCCGTGGTTGCTG
GTGGTGGGACGTCACTCGTGTGGTGTGATCATATACCACACAAGCGGAGGAATGAAGATTGCAAGCATTACC
AACACAGATGAGACCAACTGCCAGCAGATATTCTAGTTATTGTCACTCTCAGGAACGTTAGCTGACAGGCAG
GATGGGTACGTTCTCAGAAAGTGAAGGCCACCAAGTTGTACATCTCAGGTGCTGATTTCTTACCA
CAACATGACAGTAGTGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGAAGCTGCCACAGATCTGTT
CTTTGTCGTTTGGGATCCACAGGCCCTATGTATTGAAAGGAAATGTGTTGGCTCAGATCTTGTGAAACA
TATCATACAGGTTGCACTGCTGTGGTGTGATCATATACCACACAAGCGGAGGAATGAAGATTGCAAGCATTACC
GAGTGTACCCATGTTCTCAGAACAGGAGCTTCAAGCTGCAACAGGAGCTTCAAGTAAATATGCTGGCCTTCACAT
GTGAGGAAGCTTAACACTAGTTACTCTCAGAACAGGAGCTTCAAGCTGCTGAGTAATTCTCATGGTACCTTGGAAA
GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATGTCAGCCAAGAGCCTTTAT
TTGAAAGCTCATTCTTCCCAGACTTGGACTCTGGGTGAGGAGATGGGAAAGAAAGGACAGATTTCAGGAA
GAAAATCACATTGTACCTTAAACAGACTTTAGAAAAGTACAGGACTCCAATTTCAGTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAGGAAAGCTTAACACTACCTCAAGTGAACCTTATTAAAGAGAGAGAAT
CTTATGTTTAAATGGAGTTATGAAATTAAAGGATAAAAGCTTATTATACAGATGAACCAAATTAC
AAAAGTTATGAAAATTCTTATGTTACTGGGAATGATGCTCATATAAGAAATACCTTAAACTATTAAACTT
TTTATGCAAAAAGTATCTTACGTTAAATTATGATATAATCATGATTATTGTTATGTTATAATGCCAGA
TTCTTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTGACCATTTTAAATAGAAGTT
ACTTCATTATATTGACATTATTTAATAAAATGTGCAATTGAAAAAAAAAAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELQPSGVAAERPCPTTCRCLGDLDDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANIT
LLSLAGNRIEILPEHLKEFQSLETLDLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVTKLNRRNRISSAIKKMFKLQLQHLELNRNKKNVVDGLTFQQLGALKSLKMQR
NGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLGYGLLMLQELHLSQNAINRISPDAWEFC
QKLSELDLTFNHLSSLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDDLKNNEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQM
KLQLHLNTSSLLCDCQLKWLPOQVAENNFQSFVNASCAPOLLKGRSIFA VSPDGFCDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDPMTFAWKKDNELLHDAEMENYAHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTNVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRVTKGETAVLQCIAGGSPPPMLNWTKDDSPLVTERHF
FAAGNQLLIIVDSDVSVDAGKYTCEMSNTLGERGNVRLSVIPTPTCDSPQMTAPS LDDDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNL PADIPS YLSSQGTIADRO
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVYGSDPFETYHTGCSPDPRTVLMHYEPSYIKKKECYPCHSEESCERSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSCDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLD
Signal sequence:
amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGCGAGAGCGCCCAGCTGACTTGAATGGAAGGAGGCCGAGCCGGAGCGCAGCTGAGAC
TGGGGAGCGCGTTCGGCCTGTGGGCGCCGTCGGCGCCGGCGCAGCAGGGAGGGAAAGCTGTGGCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCTGGTGGTCCCCTATCCCTCTTATATA
GAAACCTTCCACACTGGGAAGGCAGCGCGAGGAGGCTCATGGTGGAGCAAGGAGGCCGCTGATCTGCAG
GCGCACAGCATTGGAGTTACAGATTTACAGATACCAATGGAAGGAGGCCAGAACAGCCTGCCTGGT
TCCATCAGCCCTGGCGCCAGCGCATCTGACTCGGCACCCCTGCAGGCACCAATGCCAGAGCCGGTGCTGC
TGCTCTGTGCTGCTGCCACAGCTGCACCTGGACCTGTGCTGCCGTGAGGGCCCCAGGATTTGGCCGAA
GTGGGGCCACAGCCTGAGCCCCGAAGAGAACGAATTGCGGAGGAGGAGCCGGTGGTACTGAGCCCTGAGG
AGCCCGGCTGCCAGCGCGTCACTGCCCCGAGACTGTGCTGTTCCAGGGCTGCTGGACTGTG
GCGGTATTGACCTGCGTGAAGTCCCGGGGACCTGCCTGAGCACACCAACCACCTATCTGAGAACACCAGC
TGGAAAAGATCTACCCCTGAGGAGCTCTCCGGTGCACCGGCTGGAGAACACTGAACCTGCAAACACCAGC
CTTCCCAGGGCTCCAGAGAAGGCGTTGAGCATCTGACCAACCTCAATTACCTGACTTGGCAATAACAAGC
TGACCTTGGCACCCGCTTCTGCCAACGCCCTGATCAGTGTGGACTTGCTGCCACTATCACCAAGATCT
ATGGGCTCACCTTGGCCAAGGCAAACCTGAGGTCTGTGACCTGACAACACAAGCTGGCAGACGCCGGC
TGCCGACAACATGTTCAACGGCTCCAGCAACGTCAGGTCTCATCTGTCCAGCAACTCCTGCGCACGTG
CCAAGCACCTGCCCTGCCCTGTAACAGCTGCACCTCAAGAACAAAGCTGGAGAAGATCCCCCGGGGCT
TCAGCGAGCTGAGCAGCCTGCGAGCTACCTGACAAACAACTACCTGACTGACGAGGGCCTGGACAACGAGA
CCTCTGGAAGCTCTCAGCCTGGAGTACCTGGATCTGTCAGCAACAACTGTCTGGTCCCAGCTGGCTGC
CGCGCAGCCTGGTGTGCTGCACTTGAGAAGAACGCCATCCGGAGGCTGGACGCGAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGTCACAGCAACCAAGCTGCCAGCAGGGCATCCACCCACTGGCCTTCCAGGGCC
TCAAGCGGTTGACACGGTGCACCTGTAACAAACAGCGCTGGAGCGCGTGCCAGTGGCCTGCCCTGCGCGTGC
GCACCCCTCATGATCCTGCACAACCAAGATCACAGCATTGGCGCGAAGACTTTGCCACCACCTACTTCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACAGGCCACAGGTGCACCGCCTCCGCAAGCTGCCCTGCTGC
GCTCGCTGGACCTGTCGGGCAACCGGGTGCACACGCTGCCACCTGGCTGCCCTGAAATGTCCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCCACAGGGCGTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCGTGCCCTGGTGGACCTGCCCATCTGAGCTGCTGGACA
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGCTCCCGAGTCACCTGAGTACCTGTACCTGAGAACAAACA
AGATTAGTGCCTGGCCGCAATGCCCTCGACTCCACGCCAACCTCAAGGGGATCTTCTCAGGTTAACAAAGC
TGGCTGTGGCTCCGTGGACAGTGCCTCCGGAGGCTGAAGCACCTGCAGGTCTGGACATTGAAGGCAACT
TAGAGTTGGTACATTCAGACATGCCAGGACCGTGGCCCTTGGGAAGGAAAGGAGGAGGAGGAGGAGGAGG
AGGAAGGAAACAAAGATAGTGAACAGGTGATGAGATGTGACCTAGGATGATGGACCGCCGACTCTTCTGC
AGCACACGCCCTGCTGCTGAGCCCCCACTCTGCCGTGTCACACAGACACACCCAGCTGCACACATGAGGCA
TCCCACATGACACGGGCTGACAGCTCATATCCCCACCCCTCCACGGCGTGTCCCACGGCCAGACACATGC
ACACACATCACACCCCTCAACACACCAACTACCTCCAACACCACAGTCTGTGTCACAC
CCCCACTACCGCTGCCACCCCTCTGAATCATGAGGGTCTGCCCTGCCACACACAGGCCACCA
TTCCCTCCCCCTGCTGACATGTGATGCTATGCAACACACCACACACATGACAAAGTCATGTGCGAA
CAGCCCTCAAAGCCTATGCCACAGACAGCTTGTGCCAGCCAGAATCAGCCATAGCAGCTGCCGTGCC
GTCCATCTGCCGTCCGTTCCCTGGAGAAGACACAAGGTATCCATGCTGTGGCCAGGTGCCCTGCC
GGAACTCACAAAAGCTGGTTTATTCTTCCATCCTATGGGACAGGCCCTCAGGACTGCTGGCCTGGCC
TGGCCACCCCTGCTCCCTCAGGTGCTGGCAGTCACCTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACCTTCCAATGGGAAGGCCAGTGGAGGAGGATGGAGAGGCCCCCTGGGTGCTGTGGGCCCTGGGG
CAGGAGTGAAGCAGAGGTGATGGGCTGGGCTGAGCCAGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTT
GTTCTCAGGCCTGTGGGGAAAGTTCGGGTGCTTTATTCTTCTAAGAAAAAAATGATAAAAT
CTCAAAGCTGATTTCTTGTATAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAA

FIGURE 108

MEGEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRSVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPEENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP
EHTNHLQLQNNQLEKIYPEELSRLHRLETLNLQNNRLTSRGLPEKAFLTNLYLYLANNK
LTLPAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLISSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPDRVTLMILHNQITGIGREDFATTYF
LEELNLSSYNRITSPOVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALA
RGALAGMAQLRELYLTSNRRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIIFRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGCGCCGCAGCAGACCTGCTCCGGCGCGCGCCTCGCCCTGTCCCTCCGGAGCGGCAG
CACTAGCCCGGGCGCGAGGGCTGGGGTTCCTCGAGACTCTCAGAGGGCGCCATCGGCCACCACCC
CAACCTGTTCCCTCGCGGCCACTCGCTCGGCCAGGACCGCTGCCAACATGGATTCTCTGGCGCTGGT
GCTGGTATCCTCGCTCACCTGCAGGGCGCCAGTCAGCAGGGAGGTGGCCAGGCAAATAGTGTATCGAT
TGGCCTATGCGTTATGGTGGAGGATGACTGCTGCTGGGCTGGCTGCCAGTCAGGGACAGTGTAGCC
TGTGTGCCAACACAGATGCAAACATGGTGAATGTATCGGCCAACACAAGTGCAAGTGTATCCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGACTGTGGCCTGAAGCCCCGGCCCTGTAAGGCACAGGTGCATGAACACTTA
CGGCAGCTACAAGTGTACTGCTCACGGATATATGCTCATGCCGGATGGTCTGCTCAAGTGCCTGACCTG
CTCCATGGCAAACATGCTAGTGGCTGTGATGTTAAAGGAAACATGGTGCAGTGCCCACCCCTGGCCT
GCACCTGGCTCCTGATGGGAGGACTGTGATGATGTAATGTGTCACAGGAAGAGCCTCCTGCCCTAGATT
TAGGAATGTGCAACACTTTGGAGCTACATGCAAGTGTATAAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTATGACATAGACGAATGCTACTGGTCAGTATCAGTGCAAGCAGCTTGCTCGATGTTAA
CGTACGTGGGCTTACAAGTGCACAGTAAAGAAGGATAACAGGGTGTGGACTGACTGTGTTATATCCAAA
AGTTATGATTGAAACCTTCAGGTCAAATTGATGACCAAGGGAAATGGTACCATTTAAAGGGTACACAGGAA
TAATAATTGGATTCTGATGTTGGAAAGTACTGTTGGCTCCGAAAGACACCATATATTCTCTATCATTACCA
CAGGCTACTCTAAGCCAACAAGACCTACACCAAGCCAACACCAATTCTACTCCACCAACCACCA
CCTGCCAACAGAGCTCGAACACCTCTACCCACCTACAACCCAGAAAGGCCAACACGGACTGACAACATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTGACACAGGGTACAGACAGACCCCTCAGAAACCCAGGG
AGATGTGTTAGTGTCTGGTACACAGTTGTAATTTGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGCCAAGGCCAGG
GGGAAAAGCTGACGCTGGTGTACCTCTCGGCCGCTCATGCATTAGGGACCTGTGCTGTCAATTGAGCA
CAAGGTGACGGGCTGACTCTGGCACACTCCAGGTGTTGTGAGAAAACACGGTGCCTCAGGAGCAGCCCTGTG
GGGAAGAAATGGTGGCATGGCTGGAGGCAAACACAGATCACCTTGCGAGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAAGGGTGGAAAAAAAGATCTATGATGGAAATTAAAGGAACACTGGATTATTGAGCTGGAGAAG
AGAAGACTGAGGGCAAACCATGATGGTTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCAGCAGCTG
TTCTCCATATGACTAAGAATAGAACAGAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTGGCAGG
GCCATTGTTAGAATACTCTATTTAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTTCTAAAAAATTAGA
TTAAATTTGCTTAAAGATGGTAAAGATGTTCTTACCCAAGGAAAAGTAACAAATTATAGAATTCCAAA
AGATGTTTGATCCTACTAGTAGTATCCAGTGGAAATCTTAAAGGCTTAATTGGACAAGGCTTAATTAGG
CATTTCCCTTGGCAATCTCTTGGAGGGGATGAAAGGGGAAGAGGCCACAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCTCTAGCAGTATTTAAAGAAAAAGGAAACTATTTATCCAAATGAGAGTATGATGGAC
AGATATTCTAGTCTCAGTATGTTCTAGTGTGGCGGTGTTTCAATGTTCTCATGGTAAAGGATATAAGCC
TTTCATTGTTCAATGGATGATGTTAGGATTTTTTTAAAGAGATCTTCAAGGAAACAGTTAGAGAG
ATTTCATCGGGTGCATTCTCTCTGCTGTGACAAGTTATCTGGCTGAGAAAGAGTGCCTGCC
ACACCGGAGACCTTCTTCCACCTCATCAGTATGATTGAGTTCTCTTCAATTGGACTCTCCAGGTTCCAC
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAAGGTCTCTGTCATTAAACCTGGTAAAGGCAGGGCTGG
AGGGGGAAAATAATCATTAAGCCTTGAGTAACGGCAGAAATATATGGCTGTAGATCCATTAAATGTT
TCCTTATGGTATATAACTGCACAGCTGAAGATGAAAGGGAAAATAATGAAAATTAACTTTGATGCTT
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTATTATTAATGTTT
CTAAAATAAAATGTTAGGGTTCCAATGGCTAATAAAAACAATTATGTAATAAAACACTGTTAGTAAT

FIGURE 110

MDFILLALVLVSSLYLQAAAEDFGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGEICGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCVDECATGRASCPFRQC
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECISLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWI PDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDN
RVQTDPQKPRGDVFSLVHSCNFDHGLCGWIREKDNDLHWEPIRD PAGGQYLTVSAAKAPGG
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGA
AATGGCTCAAGGTCTCACAACTTCCCTTGCAACAGGTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATGGCTATTGAGAGACCCA
ACAATGCCAAATACTTAAGTCTGTGGTTCTGACTTGGAAATACC
AACACAAGTCACCATGATGCCACCAATGCATCTGCTTATCAACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTAAGGTCAACATTCAAGGAAATGGAACACTATCTGCCAGTC
GAAGATACAAGTCACGGTTGATGATCCTGTCACAAAGCCAGTGGTGAGATTCATCCTCCCT
CTGGGCTGTGGAGTATGTGGGAACATGACCTGACATGCCATGTGGAAGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTT
TCCCCAAAACAATACCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAAATTACAGCT
GCCTGGTGAGGAACCTGTCAGTGAATGGAAAGTGATATCATTATGCCATCATATATT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGTGTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGCCTCGCTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAACAGAACATGGACTATGTGTGCTGTCTACACAAACATAAC
CGGCAGGCAAGATGAAACTCATTACAGTTACACTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAATCATGTACCTTAGCAAGTATAACTGGAATATCACTATTGATT
ATATCCATGTGCTTCTCTTCTATGGAAAAAATCAACCCATCAAAGTTAAAACAGAA
ACTAGAAGGCAGGCCAGAACAGAACATCAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGTGTTCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGATCGGGCAAGATTGACAGTACAGT
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATCCAGACT**GA**ACTTTCATGG
GCTAAACAGTACATTCAAGTGAAGAAATTCTGAAGAACATTAAAGGAAAACAGTGGAAAAGT
ATATTAATCTGAACTAGTGAAGAAACAGGCCAACACCTCTTACTCATTATTCTTTACA
TGCAGAAATAGAGGCATTATGCAAATTGAACACTGCAGGTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGAAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGTTCTCTCATTAAGTTGTATGAAATATCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCTGTCTCACCTACAAA
TGTGGAAACTTACATTGTTGATTTTCAGCAGACTTTGTTTATTAAATTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTATTCAAAATTCTATCTGTTATTGTACAA
CAAAGTAATAAGGATGGTGTACAAAAACAAACTATGCCCTCTTTTTTCAATCACC
AGTAGTATTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATT
TTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTTGCTTTAAAAAAAAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ
KIQVTVDPPVTKPVVQIHPPSGAVEYVGNMTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDCTSADSHPPNTYSWIRTDNTTYIIKGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTCAGTCCCCCTGGCAGTCCTGGTGTGTT
GCTTGGGGTGCTCCCTGGACGCACGGGCGGCCGGAGCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTATGCCCGTGGTGCCTGCT
TGTCAAATCTCAACCGGAATGGGAAAGTTTGCTGAATGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTATCATTGTAAGATGGTGAATTAGGCCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTATAAGTGTAAAGAGTGGAGAGTATTGAGCCCCTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTATTGAAGAACCTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCCTTGTCCCTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAAAAA
TATTATCAGAATCTGACAACCTTGAAAAAAAGTGGAGGAACAAGAGGCCGATGAAGAA
GATGTTTCAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC
CATAAAGACAAACGCTCTGGTCCATCATTGCCACAGATAATCCTAGTTAAATTTTAG
TTATCTTAATATTATGATTTGATAAAAACAGAAGATTGATCATTGTTGGTTGAAGTG
AACTGTGACTTTTGAAATATTGCAAGGTTCACTCTAGATTGTCATTAAATTGAAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTATACAAGTTGAAATATGATTTAACAGCACAGTATGATG
GTTTAAATAGTCTCTAATTGAAAGGTTCTGCAAGCAATAAGATTATGATATTGTATATTGT
TTAATAATAAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAAGTATTGCAATTAT
TGAGGTATTTAAGAAGATTATTAGAGAAAAATTCTCTCATTTGATATAATTTCCTCTG
TTCACTGTGAAAAAGAAGATATTCCATAATGGGAAGTTGCCATTGTCTCAAG
AAATGTGTTTCAGTGACAATTCTGGTCTTTAGAGGTATATTCCAAAATTCTCTGT
ATTTTTAGGTTATGCAACTAATAAAACTACCTTACATTAATTAAATTACAGTTCTACACA
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCATGGTATTCTCTGATTC
CAACAAAGTTGATTCTCTGTATTCTTACTTACTATGGGTTACATTTTATT
CAAATTGGATGATAATTCTGGAAACATTTTATGTTAGTAAACAGTATTGTTGTT
GTTTCAAACTGAAGTTACTGAGAGATCCATCAAATTGAACAATCTGTTGAATTAAAATT
TTGCCACTTTTCAGATTACATCATTCTGCTGAACATTGAAATTGTTTTTT
TTTCTTTGGATGTAAGGTGAACATTCTGATTGTTCTGATGTGAAAAAGCCTGGTA
TTTACATTGAAATTCAAAGAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAG
CATCTCTTGATATGCTTAAATGTATTGTCCTCATATAACAGAAAGTTCTTAATTGAT
TTACAGTCTGTAATGCTGATGTTAAAATAACATTATTATATTGTTAAAGACAA
ACTTCATATTATCCTGTTCTGACTGGTAATTGTTGTGGGATTACAGGTAAGA
GTCAGTAGGATGGAACATTAGTGTATTGACTCCTTAAAGAGACTAGAATACTAGTT
CACCTTAAAGAAGGGGAAACATAAAACATGAATCAACTGACCATTACGTAGTAGAC
AATTCTGTAATGTCCTCTTCTAGGCTCTGTTGCTGTGAATTGCACTAGATTACAG
TATCGTAATATAACAGTTCTTAAAGCCCTCCTTCTAGAATTAAAATATTGTACCA
AAAGAGTTGGATGTTGTAACTTGATGTCCTAGAAAAATATCCTAAGCACAAAATAAC
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTCGGGAGACCCGTATAATTGTTAACTAATTCAACAAACGGGACCCTT
CTGTGTGCCAGAAACCGCAAGCAGTGTGCTAACCCAGTGGGACAGGCAGGGATTGGAAGAGCGGG
AAGGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC
ATTGCTGATGGCCTGGTTGGTGTCTGAGCTGTGCAAGCCGAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGCCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCCGTGAATGCCTACAAACTGG
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGCAAGCGGAGTTCTTCCCCACTGATGAGGACGAGATAGG
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGGAACCTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GGCCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGGAGGAGGCACCACAAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGCTTCCAGTTGGGTGATCTGCACCGTGCCTGGAGCTCACCGCCGCTGCTC
TCCCTGACCAAGCCACGAACGAGCTGGAGGAATCTGCGGTACTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAACGCTGAGCTAGCAACCCCAGAAGGC
TCTATGAGAGGCCTGTGGACTACCTGCTGAGAGGGATGTTACGAGAGCCTCTGTCGTGG
GAGGGTGTCAAACGTACACCCCCGTAGACAGAACAGGCTTCTGTAGGTACCAACATGGCAA
CAGGGCCCCACAGCTGCTCATGGCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA
TCGTCAAGGTACTACGATGTCATGTGATGAGGAATCGAGAGGATCAAGGAGATCGCAAA
CCTAAACTGCACGAGCCACCGTCTGTGATCCAAAGACAGGAGTCCTACTGTCGCCAGCTA
CCGGGTTCCAAAAGCTCTGGCTAGAGGAAGATGATGACCCCTGTTGTGGCCGAGTAAATC
GTGGATGCAAGCATATCACAGGGTTAACAGTAAAGACTGCAAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGAGGACAGTATGAACCGCACTCGACTTCTCTAGGCGACCTTTGACAGCGG
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG
GTGGTGCCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTTGCAGGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCCTGCC
TGTGCTTGTGGCTGCAAGTGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAACGAGTTGACTGACATCCTTCTGCTCTCCCTGGTC
CTTCAGCCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCAGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCCAGCCCTCCATTAGCCTGTGCCATCCCTGGCCCAAGGCTAGGATCA
AAGTGGCTGAGCAGAGTTAGCTGTCTAGCGCTAGCAAGGTGCCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCAGTGAACCAAAGTCTGATACCTGTTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACCAAAAATAAAATGTCCCTACCAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSHVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTYQAMLSVDDCFGMGRSAYNEGDDYYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRLLSLDPSHERAGGNLR
YFEQOLLEEEEREKTLTNQTEAELATPEGIYERPVYLPERDVYESLCRGEVVKLTPRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIYRYYDVMSEEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVPDLGAAIWPKKGTAVFWYNLLRSGEDYR
TRHAACPVLVGCKWVSNKFHERGQEFLRPCGSTEVN

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTTCCTCCTTTAGTGGAAAGACAGACCATAATCCCAGTGTGAGTGAAATTGATTGT
TTCATTTATTACCGTTTGGCTGGGGTTAGTCCGACACCTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTTCTGGGATGCTGGCCTGGAAGCCAGCGGCCCTGCTCTGTCTTGGCCTCATGACCC
CAGGTCTGGTTAAAACGTAAAGCCTACTACTGGCCTGGTGCCTCATCAATCATTGATCTTGAGGCTGTGCC
CCTGGGCACCCACCTGGCAGGGCCTACCACCATTGGACTGAGCTCCCTGGCTCTGCTGCCAGCGCTTC
CCCTCATCTTAGGGCTGCTCTGGGTGCAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGGAGGGAGAAG
ATCCCTGTGTCAGGGCTGTAGGGGAGCGAGGAGGGCCACAGAACATCCAGATTGAGAGCTGCTAGACCAAAGTG
ATGAAGACTTCAAACCCCCGATTGTCCCCTACTACAGGGACCCCAACAAGCCCTACAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGCTCCCGTGGGGITGCTGGCTGTGACTCCGAGCTACACTGTCCA
CTTGCGCTGGCTGTGAAACCGTACGGTGGCCCATCACTTCCCTCGGTTACTCTACTTCAGTGGCAGCGGGGG
CCCGGGCTCCAGCAGGGATGAGCGGGCCCTGGCATGTCAGAGACCCCTGC
GCCACCTTACACACACTTGGGCCACTACGACTGGTCTCATCATGCAGGATGACACATATGTGCAGGCC
CCCGCCTGGCAGCCCTGCTGGCCACCTCAGCATCAACCAAGACCTGACTTAGGCCGGCAGAGGAGTTATTG
GCGCAGCGAGCAGGCCGGTACTGTCACTGGGGCTTGGCTACCTGGTCACTGGAGTCTCTGCTTCGTC
GGCACATCTGGATGGCTGCGAGGAGACATTCTCAGTGCCTGACGAGTGGCTGGACGCTGCTCATTTG
ACTCTCTGGCGCTGGCTGTGTCACAGCACCAGGGCAGCAGTATCGCTCATTTGAACGGCCAAAATAGGG
ACCTGAGAAGGAAGGGAGCTCGGCTTCTGAGTGCTTCGCGTGCACCCCTGCTCCGAAGGTACCCCTATGT
ACCGGCTCCACAAACGCTCAGCGCTCTGGAGTTGGAGCGGCTTACAGTGAATAGAACAACTGCAAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCTTCA
CACACACCTCGCTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGCACACCTTCTCTGTGCAGATGGGG
CTCCAAGTGCCTACAGGGGCTAGCAGGGCGACGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGCGCTATCAGCCCCGCTGCGCTCCAGAACAGCGACTGCTCAACGGCTATCGCGCTTCGACCCAGCAC
GGGCATGGAGTACACCCCTGGACCTGCTGTTGAATGTGTGACACAGCGTGGCACCAGGGCCCTGGCTCGA
GGGTCACTGCTGCGGCCACTGAGCCGGTGGAAATCCTACCTATGCCCTATGTCACTGAGGCCACCCAGTG
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGCAGCCCCGGCTTCTCGAGGCGTTGAGCCAATGTCC
TGGAGCCACGAGAACATGCAATTGCTACCCCTGCTGGCTACGGGCCACGAGAACGGTGGCGTGGAGCTCCAG
ACCCATTCTGGGTGAAGGCTGCAGCAGCGAGTTAGAGCGACGGTACCCCTGGGACGAGCTGGCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCCAGGTGCGACTCATGGACGTGGTCTCGAAGAACGACCCCTGTTGGACACTCT
TCTTCTTACCAACCGTGTGGACAAGGCCTGGGCCAGTCCACCGCTGTGCAATGCCATCTCTGGCT
GGCAGGCCCTCTTCCAGTCCATTCCAGGAGTTCAATCTGCCCTGTCACCAACAGAGATACCCCCAGGGCCCC
CGGGGGCTGGCCCTGACCCCCCCCCTCCCTGGTGTGACCCCTCCCGGGGGCTCTATAGGGGGAGATTG
ACCGCAGGCCCTGCGGAGGGCTGCTTCAACACGCTGACTACCTGGCGGGCCAGGCCGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGCTGGAGGGTGTGATGGATTTCTCTGGCTTCTCAGGGCTCC
ACCTCTTCCGGCCGTAGAGCCAGGGCTGGTGCAGAACAGTCTCCCTGCCAGACTGCAAGCCCCAGGGCTCAGTGAAG
AACTCTACCACCGCTGCCCTCAGCAACCTGGAGGGCTAGGGGGCGTGCCTGAGCTGGCTATGGCTCTTTG
AGCAGGAGCAGGCCAATAGCACTTAGCCCGCCTGGGGCCTAACCTCATTACCTTCTGCTGCTCAGCC
CCAGGAAGGGCAAGGCAAGATGGTGACAGATAAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA
ACATGTCTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLSLRLVSWIQGEGEDPCVEAVGERGGPQNPDZRARLD
QSDEDFKPRIVPYYRDPNPKYKKVLTRYIQTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSWPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPHQASRADVGALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMETYTLDDLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLPLL
VAEAAAAPAFLEAFAANVLEPREHALLTLLVYGPREGGRGAPDPFLGVAAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVSVSKHPVDTLFFLTTVWTRPGPEVLNRCRMNAISGWQAFFP
VHFQEFNPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGGLGRAQLAMALFEQEQQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCACGTGAGAGGAACCGTGCACGGCTGCCTTCCTGTCCCCAAGCC
GTTCTAGACGCCGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTTGTAAAACC
CAAAGATGTGAGTCTTGGGCTGCAGTAAAGGAGACTTGGACAAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAAC
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGTTGGAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTAATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC
CAACCAGGTAGTAGAAGGCTGTTGTTAGATATGGCTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGTATGGGTATACGCCCTAGGGCATTTGGCATATTTCAAT
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTTGTCATTATTGTAGTAGTAACATACATATCCAA
TACAGCTGTATGTTCTTTCTTAATTTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAACACATGAACATTGAAATG
TGTGGAAAGAAGTGTGTTAAGAATAATAATTTGCAAATAACTATTAAATAATATTAT
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACTTTAGCTGTGTTCCCTTACTTCTAATACTGATTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCCTCTCAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAFFSSENVKFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIEENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGSLS

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCCGCTGCCGTGGCCCTCAGCAACCCCTGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCCTCGGCTGCTGACTTCTTCTGCTGCTGCTTTCAAGGGCTGCCTGATAAGGGCTGTAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTTCATCATTACGGATTGCG
AGACAAGTGACCCCAGGATCGAGTGGAAAGAAAATCAAGATGAACAAACCACATATGTGTTTTGACAACAAAAA
TTCAAGGGAGACTTGGCGGGCTGTGCAGAAATACTGGGAAGACATCCCTGAAGATCTGAACTGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTCGTTGCTGAAATGACCGAAGGAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGGCCAGTGACCCCTGCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTG
ACTGCCAGGAGAGTGAGGGCCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCGTACGCCACGGATT
CCAGGCAATCCAGATTCTCGCAATTCTTCCACTTAAACTCTGAAACAGGCACITGGTGTTCAGTGC
TTCAAGGAGACTCTGGCGACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTCTGGTTGCTCTGCTGTACTGCCCTGA
TCACGTTGGGCATCTGCTGTGCATAACAGACGGCTACTTCATCAACAATAACAGGATGGAGAAAGTTACAAGA
ACCCAGGAAACCAAGATGGAGTTAACTACATCCGCACTGAGGAGGGCACTTCAGACACAAGTCATCGTTTG
TGATTGAGACCCCGGGTGTGGCTGAGAGCGCACAGAGCGCACGTGACATACCTCTGCTAGAAACTCTGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAAAGAGCTTTCGTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAAATATAACCACAA
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGCTTAACTCTGTTCTGAGTATTAGG
GTGATCTTAAAGAGTTGCTCACGTAACGCCGTGCTGGGCCCTGTAAGGCCAGCATGTTACCAACTGGTGT
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCCAGCAGCGCATCCGGCGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTCTTAAAGGCTCTG
TGATCGGTGTTGCACTGTCATTGTGGAGAAGCTTTGGATCAGCATTGTAAGGAAACAAACCAAAATCAGGAAG
GTAAATTGGGTGCTGGAAGAGGGATCTTGCCTGAGGAACCCCTGTTGCTTCAACAGGGTGTCAAGGATTAAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTCTATGGGTCTGTTTATTAAAGGCTTAA
TACATCTAAATTGGCTAAGGATGTATTGATTATTGAAAAGAAAATTCTATTAAACTGTAATATATTGT
CATACAATGTTAAATAACCTATTGGGTTAAAGGTTCAACTTAAGGTTAGAAGTCTCAAGCTACTAGTGTAAAT
TGGAAAATATCAATAATTAGAGTATTGACCAAGGAATTCTCATGGAAGTTACTGTGATGTTCTTTCT
CACACAAGTTTACGCTTTCACAAGGAACCTACACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAATTCAGGTTAAGCAATGTTGAAATCAGTTGCTCTTCAAAGAAACCTCTCAGGTTAGCTTGA
GCCTCTCTGAGATGACTAGGACAGTCTGTAACCCAGAGGGCACCCAGAAGGCCCTCAGATGTACATACAGATG
CCAGTCAGCTCCTGGGGCTTGCAGGCCAGGCCAGCCCTCTAGCTCACTGTTGCCCTGCTGTGCCAGGAGGCC
GCCATCCTGGGGCTTGCAGTGGCTGTCTCCAGTGAGCTTACTCAGTGGCCCTGCTTCACTCAGCAGCAGC
TCTCAGGTGGCACTGCAGGGACACTGGTGTCTCCATGTAGCGTCCAGCTTGGCTCTGTAACAGACCTCT
TTTGGTTATGGATGGCTCACAAAATAGGGCCCCAATGCTATTGTTTTAAGTTGTTAATTATTGTT
AAGATTGCTAAGGCCAAGGAATTGCAAAATCAAGTCTGCAAGTACAATAACATTAAAAGAAAATGGAT
CCCACGTGTTCTCTTGCACAGAGAAAGCACCAGACGCCACAGGCTCTGCGATTCTCAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGGCTTTAAAGAACGTCAGGTGGAGCAGCAGGTGAAGGGCTGGCGGGGAGGAAAG
TGAAACGCCTGAATCAAAAGCAGTTCTAATTGACTTTAATTTCTACCGCCGGAGACACTGCTCCATT
TGTGGGGGGACATTAGCAACATCACTCAGAAGCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCC
GCCGTGCTGGACTCAGGACTGAAGTGTGAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGCTGG
GAATGGCTCTCACTACTCACCTTGTCTTCAAGCTTCAAGTGTCTGGTTTTTAACTTTGACAGCTTTTTT
AATTGCTACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGCCCCAGGCCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGTCTGCCCTGGCTGCTGCATGGCATTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTTGGGGATTCA
CTTGGTTGTCATAGTGTAGGGTAGGCTTATTGCCCCCTTCTTATACCTAAACCTCTACACTAGTGC
TGGGAAACAGGCTGAAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTGAAAGATATGAATGTGACTCAAGACTCGAGGGCAGACGGCTGTGATTCT
GCCTTGGATGGATGGATGGCTGTACACAGATGCTACAGACTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTTATAAAAGCTTCAAAAAACCCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLFLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267